

18561
SEARCH REQUEST FORM

Examiner # (Mandatory): _____ Requester's Full Name: _____

Art Unit _____ Location (Bldg/Room#): _____ Phone (circle 305 306 308) _____

Serial Number: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

Title of Invention _____

Inventors (please provide full names): _____

Earliest Priority Date: _____

Keywords (include any known synonyms registry numbers, explanation of initialisms): _____

Search Topic:

Please write detailed statement of the search topic, and the concept of the invention. Describe as specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc., if known. You may include a copy of the abstract and the broadcast or most relevant claim(s).

BEST AVAILABLE COPY

STAFF USE ONLYSearcher: JanSearcher Phone #: 4498

Searcher Location: _____

Date Picked Up: 8/21/99Date Completed: 8/23/99Clerical Prep Time: 60 / 90Terminal Time: 30 / 90Number of Databases: 11**Type of Search** _____ **Vendors (include cost where applicable)** _____☒ N.A. Sequence X4 _____ STN☒ A.A. Sequence X10 _____ Questel/Orbit

_____ Structure (#) _____ Lexis/Nexis

_____ Bibliographic _____ WWW/Internet

_____ Litigation1 ☒ In-house sequence systems (list)

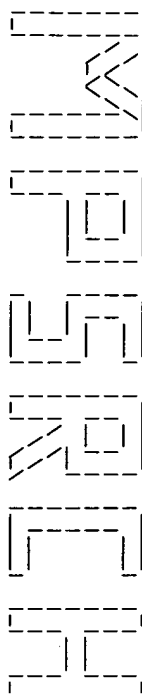
_____ Fulltext _____ Dialog

_____ Procurement _____ Dr. Link

_____ Other _____ Westlaw

_____ Other (specify) _____

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Msearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Sat Aug 21 12:10:37 1999; Maspar time 18.24 Seconds
Tabular output not generated.

Title: >US-09-219-935-5
Description: (1-446) from US09219935.pep
Perfect Score: 446
Sequence: 1 MANLVLSEGCIRPLPRITYT.....EVVYKADPNLXGEVKRAD 446

Scoring table: TABLE uniprottable
Gap 60

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr60
1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 3.698; Variance 0.462; scale 8.000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	446	100.0	446	2	JO2336 omega-3 fatty acid de	0.00e+00
2	103	23.1	404	2	PG0812 omega-3 fatty acid de	1.77e-300
3	43	9.6	398	2	TO1696 omega-3 fatty acid de	7.85e-103
4	40	9.0	441	2	TO3029 omega-3 fatty acid de	2.65e-93
5	36	8.1	443	2	TO1697 omega-3 fatty acid de	1.04e-80
6	36	8.1	453	2	JO2339 omega-3 fatty acid de	5.10e-56
7	28	6.3	377	2	JO2337 omega-3 fatty acid de	5.10e-56
8	28	6.3	383	2	AA4227 omega-3 fatty acid de	5.10e-56
9	28	6.3	386	2	JO2335 omega-3 fatty acid de	5.10e-56
10	27	6.1	380	2	JO2338 omega-3 fatty acid de	5.41e-53
11	24	5.4	379	2	UC2555 omega-3 fatty acid de	5.04e-44
12	16	3.6	359	2	S52650 omega-3 fatty acid de	3.19e-21
13	16	3.6	429	2	SO1919 probable ribosomal pr	6.82e-02
14	8	1.8	429	2	SO1919 knitrp protein - fru	6.82e-02
15	8	1.8	598	2	S65770 maltooligosyltrehalos	6.82e-02
16	7	1.6	113	2	A60887 synuclein - Pacific e	4.99e+00
17	7	1.6	158	2	DV1111 hypothetical protein	4.99e+00
18	7	1.6	193	2	S67699 probable membrane pro	4.99e+00
19	7	1.6	212	2	F71182 hypothetical protein	4.99e+00
20	7	1.6	213	2	S08313 abscisic acid-induced	4.99e+00
21	7	1.6	257	2	D70341 hypothetical protein	4.99e+00
22	7	1.6	257	2	S16865 gene f41 protein - mo	4.99e+00
23	7	1.6	305	2	AV0212 conserved hypothetical	4.99e+00

24	7	1.6	326	2	S34427	tristetraproline prot	4.99e+00
25	7	1.6	329	1	VGXRC2	glycoprotein VP7 prec	4.99e+00
26	7	1.6	332	2	A57140	mcb protein homolog	4.99e+00
27	7	1.6	337	2	A54214	petalene synthase	4.99e+00
28	7	1.6	367	1	WOHU	alpha-2-HS-glycoprote	4.99e+00
29	7	1.6	388	1	S72995	alanine racemase (EC	4.99e+00
30	7	1.6	389	2	F69366	conserved hypothetical	4.99e+00
31	7	1.6	388	2	D40785	hypothetical protein,	4.99e+00
32	7	1.6	415	1	C64473	adenosylhomocysteinas	4.99e+00
33	7	1.6	468	2	A64956	flagellar hook-associ	4.99e+00
34	7	1.6	481	2	A56346	transcription factor	4.99e+00
35	7	1.6	555	2	I51671	Weela kinase - Africa	4.99e+00
36	7	1.6	649	2	S67867	hypothetical protein	4.99e+00
37	7	1.6	733	2	S78376	photosystem I P700 ap	4.99e+00
38	7	1.6	741	1	S20923	photosystem I protein	4.99e+00
39	7	1.6	754	2	S61113	YRA6 protein - yeast	4.99e+00
40	7	1.6	790	2	G02678	cadherin-14 - human	4.99e+00
41	7	1.6	792	2	S63141	hypothetical protein	4.99e+00
42	7	1.6	809	2	A46747	Na+/H+-exchanging pro	4.99e+00
43	7	1.6	918	2	S04255	regulatory protein qa	4.99e+00
44	7	1.6	1065	2	E69795	acriflavin resistance	4.99e+00
45	7	1.6	2038	2	A43742	female sterile homoot	4.99e+00

ALIGNMENTS

RESULT 1
ENTRY 1
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CFD -
ORGANISM Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
cress

DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999

ACCESSIONS
REFERENCE
#authors
JO2336 A49503
JO2335

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession JO2336
#molecule_type mRNA
#residues 1-446 #label YAD

REFERENCE
#authors Iba, K.; Gibson, S.; Nishitani, T.; Fuse, T.; Nishimura, M.;
Arondel, V.; Hugly, S.; Somerville, C.

#journal J. Biol. Chem. (1993) 268:24099-24105
#title A gene encoding a chloroplast omega-3 fatty acid desaturase
complements alterations in fatty acid desaturation and
chloroplast copy number of the fat7 mutant of Arabidopsis
thaliana.
#cross-references MUID:94043239

#accession A49503
#status preliminary
#molecule_type DNA
#residues 1-446 #label IBA
#cross-references GB:J14007; MID:9461160; PID:94541653
sequence extracted from NCBI backbone (NCBIN:139485,
NCBIP:139486)

COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase

SUMMARY #length 446 #molecular-weight 51174 #checksum 4653
Query Match 100.0%; Score 446; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 446: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Db 1 MANLVSECGIRPLEPRIYTPRNSFLSNKKFRPSLSSSYKTSPLSFGINSRDGFTTR 60
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-404 #label YAD
#cross-references GB:L22963
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 404 #molecular-weight 46617 #checksum 9400

Query Match 23.1%; Score 103; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.77e-300;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 265 IPYWINVMDLVYTLHHGHEDKLPWYRGKMSYLRGGLTTLDRDYGILNNIHHIDISTH 324
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-404 #label YAD
#cross-references GB:L22963
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 404 #molecular-weight 46617 #checksum 9400

Query Match 23.1%; Score 103; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.77e-300;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPYWINVMDLVYTLHHGHEDKLPWYRGKMSYLRGGLTTLDRDYGILNNIHHIDISTH 366
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-404 #label YAD
#cross-references GB:L22963
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 404 #molecular-weight 46617 #checksum 9400

Query Match 23.1%; Score 103; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.77e-300;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 325 VHHHFPQIPHYHLVTEAKRPVLGKYRREPKSGPLPHLL 367
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-404 #label YAD
#cross-references GB:L22963
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 404 #molecular-weight 46617 #checksum 9400

QY 367 VHHHFPQIPHYHLVTEAKRPVLGKYRREPKSGPLPHLL 409
RESULT 3
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#accession
#status
#molecule_type mRNA
#residues 1-441 #label HAM
#cross-references EMBL:D79979; NID:d1093316; PID:g1694625
#experimental_source cultivar SRI
GENETICS
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 441 #molecular-weight 50310 #checksum 6941

Query Match 9.0%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.65e-93;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 355 INNHHIDIGTHVHHLFQIPHYHLVTEAKRPVLGKY 394
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-441 #label HAM
#cross-references EMBL:D79979; NID:d1093316; PID:g1694625
#experimental_source cultivar SRI
GENETICS
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 441 #molecular-weight 50310 #checksum 6941

Query Match 9.0%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.65e-93;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 INNHHIDIGTHVHHLFQIPHYHLVTEAKRPVLGKY 395
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-441 #label HAM
#cross-references EMBL:D79979; NID:d1093316; PID:g1694625
#experimental_source cultivar SRI
GENETICS
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 441 #molecular-weight 50310 #checksum 6941

Query Match 9.0%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.65e-93;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-441 #label HAM
#cross-references EMBL:D79979; NID:d1093316; PID:g1694625
#experimental_source cultivar SRI
GENETICS
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 441 #molecular-weight 50310 #checksum 6941

Query Match 9.0%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.65e-93;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 EMSYLRGGLTTLDRDYGILNNIHHIDIGTHVHHLFQIPHYHL 333
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-398 #label BER
#cross-references EMBL:D63953; NID:d1164452; PID:d1023305
#experimental_source strain honey bantum
GENETICS
KEYWORDS
SUMMARY #length 398 #checksum 5580

Query Match 9.6%; Score 43; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.85e-103;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 EMSYLRGGLTTLDRDYGILNNIHHIDIGTHVHHLFQIPHYHL 380
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-398 #label BER
#cross-references EMBL:D63953; NID:d1164452; PID:d1023305
#experimental_source strain honey bantum
GENETICS
KEYWORDS
SUMMARY #length 398 #checksum 5580

Query Match 9.6%; Score 43; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.85e-103;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 EMSYLRGGLTTLDRDYGILNNIHHIDIGTHVHHLFQIPHYHL 333
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-398 #label BER
#cross-references EMBL:D63953; NID:d1164452; PID:d1023305
#experimental_source strain honey bantum
GENETICS
KEYWORDS
SUMMARY #length 398 #checksum 5580

Query Match 9.6%; Score 43; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.85e-103;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 EMSYLRGGLTTLDRDYGILNNIHHIDIGTHVHHLFQIPHYHL 380
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:94302147
#accession
#molecule_type mRNA
#residues 1-398 #label BER
#cross-references EMBL:D63953; NID:d1164452; PID:d1023305
#experimental_source strain honey bantum
GENETICS
KEYWORDS
SUMMARY #length 398 #checksum 5580

Query Match 9.6%; Score 43; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.85e-103;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize
ORGANISM #formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
ACCESSIONS T01697
REFERENCE 214400
#authors Berserich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;
Kusano, T.
#journal Plant Mol. Biol. (1998) 36:297-306
#title Two maize genes encoding omega-3 fatty acid desaturase and
their differential expression to temperature.
#accession T01697
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-443 #label BER
#cross-references EMBL:D63954; NID:d1164453; PID:d1023306
#experimental_source strain honey bantam
GENETICS
#gene FAD7
#introns 163/2; 193/2; 215/3; 246/3; 308/3; 335/3; 381/3
KEYWORDS oxidoreductase
SUMMARY #length 443 #molecular_weight 49437 #checksum 8872
Query Match 8.1%; Score 36; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 1.04e-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 317 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 352
QY 319 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 354
RESULT 6
ENTRY J02339 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
ACCESSIONS J02339
REFERENCE J02335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents cDNA:GMD
#accession J02339
#molecule_type mRNA
#residues 1-453 #label VAD
#cross-references GB:L122965; NID:q408791; PID:q408792
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 453 #molecular_weight 51362 #checksum 7549
Query Match 8.1%; Score 36; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.04e-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 327 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 362
QY 319 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 354
RESULT 7
ENTRY J02337 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BN3 - rape
ORGANISM #formal_name Brassica napus #common_name rape

DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
ACCESSIONS J02337
REFERENCE J02335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents cDNA:BN3
#accession J02337
#molecule_type mRNA
#residues 1-377 #label VAD
#cross-references GB:L122962; NID:q408491; PID:q408492
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 377 #molecular_weight 43258 #checksum 3294
Query Match 6.3%; Score 28; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 5.10e-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 117 ILVPHGWRISHRTHQNHGVNDESW 144
QY 188 ILVPHGWRISHRTHQNHGVNDESW 215
RESULT 8
ENTRY A44227 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - rape
ALTERNATE_NAMES omega-3 linoleate desaturase
ORGANISM #formal_name Brassica napus #common_name rape
DATE 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
ACCESSIONS A44227
REFERENCE A44227
#authors Arondel, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman,
H.M.; Somerville, C.R.
#journal Science (1992) 258:1353-1355
#title Map-based cloning of a gene controlling omega-3 fatty acid
desaturation in Arabidopsis.
#cross-references MUID:93088059
#accession A44227
#status preliminary; not compared with conceptual translation
#molecule_type nucleic acid
#residues 1-383 #label ANO
#cross-references GB:L01418; NID:g167147; PID:g167148
#experimental_source developing seed
#note sequence extracted from NCBI backbone (NCBIP:119842)
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 383 #molecular_weight 43936 #checksum 2897
Query Match 6.3%; Score 28; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 5.10e-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 123 ILVPHGWRISHRTHQNHGVNDESW 150
QY 188 ILVPHGWRISHRTHQNHGVNDESW 215

RESULT 9
ENTRY J02335 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 -
Arabidopsis thaliana
ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear

DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
12-Mar-1999
ACCESSIONS J02335; J02487
REFERENCE J02335
#authors Yaday, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession J02335
#molecule_type mRNA
#residues 1-386 #label YAD
REFERENCE 214675
#authors Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, F.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
J.C.
#submission Submitted to the EMBL Data Library, August 1998
#description Arabidopsis thaliana chromosome II BAC F3F1 genomic
sequence.
#accession T02487
#status Translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-386 #label ROU
#cross-references EMBL:AC004680; NID:g3420043; PID:g3420053
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.

GENETICS
#map_position II
#introns 103/2; 133/2; 155/3; 186/3; 248/3; 275/3; 321/3
#note F23F1.10
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 386 #molecular-weight 44076 #checksum 8044

Query Match 5.3%; Score 28; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 5.10e-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 ILVPHGWRISHRTGHQNHGHVDESW 153
|||||
QY 188 ILVPHGWRISHRTGHQNHGHVDESW 215

RESULT 10
ENTRY J02338 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GM3 - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999
ACCESSIONS J02338
REFERENCE J02335
#authors Yaday, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession J02338
#molecule_type mRNA
#residues 1-380 #label YAD
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase; transmembrane protein
SUMMARY #length 380 #molecular-weight 44185 #checksum 1659

Query Match 6.1%; Score 27; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.41e-53;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 295 NHHHDIGTHVHHLFPQIPHYLVEAT 321
|||||
QY 358 NHHHDIGTHVHHLFPQIPHYLVEAT 384

RESULT 11
ENTRY JC2555 #type complete
TITLE omega-3 fatty acid desaturase - common tobacco (cv. SR1)
ORGANISM #formal_name Nicotiana tabacum #common_name common tobacco
DATE 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change
24-Sep-1998
ACCESSIONS JC2555
REFERENCE JC2555
#authors Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Gene (1994) 147:293-294
#title Cloning of a cDNA encoding tobacco omega-3 fatty acid
desaturase.
#cross-references MUID:95011632
#accession JC2555
#status Preliminary
#molecule_type mRNA
#residues 1-379 #label HAM
#cross-references DBJ:J26509; NID:g1311480; PID:d106059; PID:g599592
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
SUMMARY #length 379 #molecular-weight 44149 #checksum 1940

Query Match 5.4%; Score 24; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 5.04e-44;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 NHHHDIGTHVHHLFPQIPHYL 314
|||||
QY 357 NHHHDIGTHVHHLFPQIPHYL 380

RESULT 12
ENTRY S52650 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - Synechocystis
ORGANISM #formal_name Synechocystis sp.
DATE 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
17-Mar-1999
ACCESSIONS S52650; S75843
REFERENCE S52649
#authors Sakamoto, T.; Ios, D.A.; Higashi, S.; Wada, H.; Nishida, I.;
Ohmori, M.; Murata, N.
#journal Plant Mol. Biol. (1994) 26:249-263
#title Cloning of omega-3 desaturase from Cyanobacteria and its use
in altering the degree of membrane-lipid unsaturation.
#cross-references MUID:95035996
#accession S52650
#molecule_type DNA
#residues 1-359 #label SAK
#cross-references GB:D13780; NID:g600596; PID:d1003430; PID:g600598
#note the authors translated the initiation codon GTG for
residue 1 as Val

REFERENCE S74322
#authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugita, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Natsu, K.; Okumura, S.; Shimpo,
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.

#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
#cross-references MWID:97061201
#accession S75843
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-359 ##label KAN
#cross-references EMBL:D99913; GB:AB001339; NID:91653348; PID:d1019035; PID:91653388
#note the nucleotide sequence was submitted to the EMBL Data Library, June 1996

GENETICS
#start codon GTG
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 359 #molecular-weight 41919 #checksum 9162

Query Match
Best Local Similarity 100.0%; Pred. No. 3.19e-21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPHGWRISHRTH 129
114 ILVPHGWRISHRTH 203

RESULT 13
ENTRY H71349 #type complete
TITLE Probable ribosomal protein L1 (rplA) - syphilis spirochete
ORGANISM #formal_name Treponema pallidum subsp. pallidum #common_name syphilis spirochete
DATE 24-Jul-1998 #sequence-revision 24-Jul-1998 #text-change 17-Mar-1999

ACCESSIONS H71349
REFERENCE A71250
#authors Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, M.; Hickey, E.K.; Clayton, R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod, M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonald, L.; Artach, P.; Bowman, C.; Cotton, M.D.; Fujii, C.; Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Matthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
#journal Science (1998) 281:375-388
#title Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
#cross-references MWID:98332770
#accession H71349
#status preliminary; nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-226 ##label COL
#cross-references GB:AE001205; GB:AE000520; NID:93322501; PID:93322508
#experimental_source strain Nichols

GENETICS
#gene TP0238
CLASSIFICATION #superfamily Escherichia coli ribosomal protein L1
SUMMARY #length 226 #molecular-weight 24977 #checksum 6350

Query Match
Best Local Similarity 100.0%; Pred. No. 6.82e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 83 ALAAGAY 90
130 ALAAGAY 137

RESULT 14
ENTRY S01919 #type complete

TITLE knirps protein - fruit fly (*Drosophila melanogaster*)
ORGANISM #formal_name *Drosophila melanogaster*
DATE 31-Dec-1990 #sequence-revision 31-Dec-1990 #text-change 24-Sep-1998
ACCESSIONS S01919; S02057
REFERENCE S01919
#authors Nauber, U.; Pankratz, M.J.; Kienlin, A.; Seifert, E.; Klemm, U.; Jaekle, H.
#journal Nature (1988) 336:489-492
#title Abdominal segmentation of the *Drosophila* embryo requires a hormone receptor-like protein encoded by the gap gene knirps.
#cross-references MWID:89057148
#accession S01919
#molecule-type DNA
#residues 1-429 ##label NAU1
REFERENCE S02057
#authors Nauber, U.
#submission submitted to the EMBL Data Library, October 1988
#accession S02057
#molecule-type DNA
#residues 1-106, 'L', 108-429 ##label NAU2
#cross-references EMBL:X13331; NID:98153; PID:98154

GENETICS
#gene knirps
#cross-references FlyBase:FBgn0001320
#introns 26/3
KEYWORDS DNA binding; nucleus; transcription regulation; zinc finger
SUMMARY #length 429 #molecular-weight 45585 #checksum 9430

Query Match
Best Local Similarity 100.0%; Pred. No. 6.82e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 288 TSSSPLSF 295
43 TSSSPLSF 50

RESULT 15
ENTRY S65770 #type complete
TITLE maltoligosyltrehalose trehalohydrolase - *Arthrobacter* sp. (strain Q36)
ORGANISM #formal_name *Arthrobacter* sp.
DATE 28-Oct-1996 #sequence-revision 13-Mar-1997 #text-change 18-Sep-1998
ACCESSIONS S65770
REFERENCE S65769
#authors Maruta, K.; Hattori, K.; Nakada, T.; Kubota, M.; Sugimoto, T.; Kurimoto, M.
#journal Biochim. Biophys. Acta (1996) 1289:10-13
#title Cloning and sequencing of trehalose blosynthesis genes from *Arthrobacter* sp. Q36.
#cross-references MWID:96195835
#accession S65770
#status preliminary
#molecule-type DNA
#residues 1-598 ##label MAR
#cross-references EMBL:D63343; NID:91255444; PID:d1010313; PID:91255446
CLASSIFICATION #superfamily trehalose trehalohydrolase
SUMMARY #length 598 #molecular-weight 65831 #checksum 4532

Query Match
Best Local Similarity 100.0%; Pred. No. 6.82e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

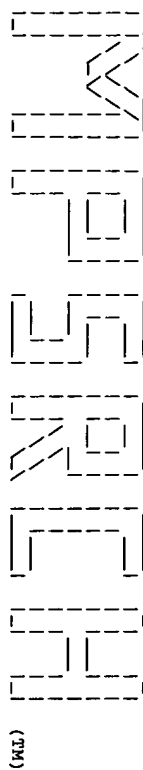
Db 8 EAKPYVG 15
385 EAKPYVG 392

Mon Aug 23 09:46:21 1999

US-09-219-935-5.rpt

Page 6

Search completed: Sat Aug 21 12:11:46 1999
Job time : 69 secs.


 (TM)

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Msparh_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:12:03 1999; MasPar time 12.66 Seconds

Tabular output not generated. 996.213 Million cell updates/sec

Title: >US-09-219-935-5
 Description: (1-446) from US09219935.pep
 Perfect Score: 446
 Sequence: 1 MANVLSCGIRPLPRITTT.....EVVYKADPNLXGEVKEVRAD 446

Scoring table: TABLE uniprottable
 Gap 60

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 3.773; Variance 0.430; scale 8.776

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	446	100.0	446	1	FD3C_ARATH OMEGA-3 FATTY ACID DES	0.00e+00
2	103	23.1	404	1	FD3C_BRANA OMEGA-3 FATTY ACID DES	0.00e+00
3	44	9.9	460	1	FD3C_RICCO OMEGA-3 FATTY ACID DES	5.10e-116
4	43	9.6	435	1	FD3D_ARATH TEMPERATURE-SENSITIVE	1.58e-112
5	36	8.1	447	1	FD3C_SESIN OMEGA-3 FATTY ACID DES	2.56e-88
6	36	8.1	453	1	FD3C_SOYBN OMEGA-3 FATTY ACID DES	2.56e-88
7	28	6.3	377	1	FD3J_BRANA OMEGA-3 FATTY ACID DES	2.56e-61
8	28	6.3	383	1	FD3J_BRANA OMEGA-3 FATTY ACID DES	2.56e-61
9	28	6.3	386	1	FD3E_ARATH OMEGA-3 FATTY ACID DES	2.56e-61
10	27	6.1	380	1	FD3E_SOYBN OMEGA-3 FATTY ACID DES	5.18e-58
11	25	5.6	380	1	FD3E_PHAU OMEGA-3 FATTY ACID DES	1.86e-51
12	24	5.4	379	1	FD3E_TOBAC OMEGA-3 FATTY ACID DES	3.27e-48
13	8	1.8	226	1	R1L_TREPA 50S RIBOSOMAL PROTEIN	2.29e-02
14	8	1.8	429	1	KNIR_DROME ZIGOTIC GAP PROTEIN KN	2.29e-02
15	7	1.6	85	1	SYU_TORCA 50S RIBOSOMAL PROTEIN	2.28e+00
16	7	1.6	143	1	SYU_TORCA 50S RIBOSOMAL PROTEIN	2.28e+00
17	7	1.6	172	1	YVT6_YEAST HYPOTHETICAL 19.2 KD P	2.28e+00
18	7	1.6	213	1	LEAL_HORVU ABA-INDUCIBLE PROTEIN	2.28e+00
19	7	1.6	232	1	Y08E_MYCU HYPOTHETICAL 23.9 KD P	2.28e+00
20	7	1.6	257	1	BR4L_MOUSE BRAIN PROTEIN F41.	2.28e+00
21	7	1.6	326	1	TTP_HUMAN TRISTERAROLINE (TTP)	2.28e+00
22	7	1.6	329	1	VS09_ROTSC GLYCOPROTEIN VP7 (SERO	2.28e+00
23	7	1.6	336	1	PLTS_STRSC PENTALENE SYNTHASE (2.28e+00

24	7	1.6	367	1	A2HS_HUMAN ALPHA-2-HS-GLYCOPROTEIN	2.28e+00
25	7	1.6	388	1	YC09_KLEPN HYPOTHETICAL 44.6 KD P	2.28e+00
26	7	1.6	388	1	ALR_MYCLE ALANINE RACEMASE (EC 5	2.28e+00
27	7	1.6	389	1	YP46_RTBVP ALANINE RACEMASE (EC 5	2.28e+00
28	7	1.6	389	1	ALR_MYCSH ALANINE RACEMASE (EC 5	2.28e+00
29	7	1.6	415	1	SAHH_METJA ADENOSYLHOMOCYSTEINASE	2.28e+00
30	7	1.6	417	1	RBL_ACRAV RIBULOSE BISPHOSPHATE	2.28e+00
31	7	1.6	467	1	FLID_ECOLI FLAGELLAR HOOK-ASSOCIA	2.28e+00
32	7	1.6	470	1	EZF_HUMAN EPITHELIAL ZINC-FINGER	2.28e+00
33	7	1.6	474	1	EZF_MOUSE GUT ENRICHED KRUPPEL-L	2.28e+00
34	7	1.6	481	1	KNIR_DROVI ZIGOTIC GAP PROTEIN KN	2.28e+00
35	7	1.6	555	1	WEEL_XENLA WEEL-LIKE PROTEIN KINA	2.28e+00
36	7	1.6	733	1	PSAB_ODOSI PHOTOSYSTEM I P700 CHL	2.28e+00
37	7	1.6	740	1	PSAB_SYNEN PHOTOSYSTEM I P700 CHL	2.28e+00
38	7	1.6	742	1	PSAB_MASIA PHOTOSYSTEM I P700 CHL	2.28e+00
39	7	1.6	790	1	CADE_HUMAN CAHERIN-14 PRECURSOR.	2.28e+00
40	7	1.6	792	1	UBPA_YEAST UBIQUITIN CARBOXYL-TER	2.28e+00
41	7	1.6	809	1	NAH2_RABIT SODIUM/HYDROGEN EXCHAN	2.28e+00
42	7	1.6	918	1	QA1S_NEUCR OUTINATE REPRESSOR.	2.28e+00
43	7	1.6	946	1	YBT6_YEAST HYPOTHETICAL 105.9 KD	2.28e+00
44	7	1.6	1045	1	Y052_HUMAN HYPOTHETICAL PROTEIN K	2.28e+00
45	7	1.6	2038	1	FSH_DROME FEMALE STERILE HOMEOITI	2.28e+00

ALIGNMENTS

RESULT	ID	SEQUENCE	STANDARD	PRT	446 AA.
1	FD3C_ARATH	MANVLSCGIRPLPRITTT.....EVVYKADPNLXGEVKEVRAD 446			
AC	P46310;				
DT	01-NOV-1995 (REL. 32, CREATED)				
DT	01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)				
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)				
DE	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).				
GN	PNP7 OR PNP7.				
OS	ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).				
OG	CHLOROPLAST.				
OC	EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;				
OC	EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;				
OC	CAPRALES; BRASSICACEAE; ARABIDOPSIS.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;				
RX	MDLINE; 94032147.				
RA	YDVAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,				
RA	KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWENGER B., STECCA K.L.,				
RA	ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,				
RA	FELDMANN K.A., PIERCE J., BROWSE J.,				
RT	"Cloning of higher plant omega-3 fatty acid desaturases.";				
RL	PLANT PHYSIOL. 103:467-476(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-CV. COLUMBIA; TISSUE-AERIAL PARTS;				
RX	MDLINE; 94043239.				
RA	IBA K., GIBSON S., NISHICHI T., FUSE T., NISHIMURA M., ARONDEL V.,				
RA	HIGLY S., SOMERVILLE C.R.,				
RT	"A gene encoding a chloroplast omega-3 fatty acid desaturase				
RT	complements alterations in fatty acid desaturation and chloroplast				
RT	copy number of the faty mutant of Arabidopsis thaliana.";				
RL	J. BIOL. CHEM. 268:24099-24105(1993).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;				
RA	WATAHAKI M., YAMAMOTO K.,				
RA	SUBMITTED (NOV-1993) TO EMBL/GENBANK/DBJ DATA BANKS.				
CC	-1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES				
CC	THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY				
CC	ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT				
CC	TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS				
CC	ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.				
CC	-1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.				
CC	-1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).				
CC	-1- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS.				
CC	-1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE				

CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L22961; G408481; -
DR EMBL: D14007; G541553; -
DR EMBL: D26019; G468434; -
DR PFM: PF00487; FA.desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT TRANSIT 1 ?
FT CHAIN 1 ?
FT CHLOROPLAST (POTENTIAL)
FT OMEGA-3 FATTY ACID DESATURASE,
FT CHLOROPLAST.
FT DOMAIN 163 167 HISTIDINE BOX 1.
FT DOMAIN 199 203 HISTIDINE BOX 2.
FT DOMAIN 366 370 HISTIDINE BOX 3.
SQ SEQUENCE 446 AA; 51174 MW; 8DE08779 CRC32;

Query Match 100.0%; Score 446; DB 1; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MANVLVSCGRPLPRITTPRSNPLSNKFRPSLSSSYKTSSTSPFLNSRDGTR 60
QY 1 MANVLVSCGRPLPRITTPRSNPLSNKFRPSLSSSYKTSSTSPFLNSRDGTR 60
Db 61 NMANLVSTPLTPFEESPLEEDNKORFPGAPPFNLADIIRAIIPKHCWKNPKMSLSY 120
QY 61 NMANLVSTPLTPFEESPLEEDNKORFPGAPPFNLADIIRAIIPKHCWKNPKMSLSY 120
Db 121 VVRDVAIYFALAAGAAATYNNITWPLVLAOGTFMVALFVGHDCGSGESNDPKLSNV 180
QY 121 VVRDVAIYFALAAGAAATYNNITWPLVLAOGTFMVALFVGHDCGSGESNDPKLSNV 180
Db 121 VVRDVAIYFALAAGAAATYNNITWPLVLAOGTFMVALFVGHDCGSGESNDPKLSNV 180
QY 121 VVRDVAIYFALAAGAAATYNNITWPLVLAOGTFMVALFVGHDCGSGESNDPKLSNV 180
Db 181 GHLLHSSTLVYHGWRISHTRHONHGHVENDSWHPKSEKIYNTLDKPTFFRFTPLV 240
QY 181 GHLLHSSTLVYHGWRISHTRHONHGHVENDSWHPKSEKIYNTLDKPTFFRFTPLV 240
Db 181 GHLLHSSTLVYHGWRISHTRHONHGHVENDSWHPKSEKIYNTLDKPTFFRFTPLV 240
QY 181 GHLLHSSTLVYHGWRISHTRHONHGHVENDSWHPKSEKIYNTLDKPTFFRFTPLV 240
Db 241 MLAYPFYLMASPKGKSHYHPDSDLFLPKERKVDLTSTACWTAAALVCLNTFIFIQ 300
QY 241 MLAYPFYLMASPKGKSHYHPDSDLFLPKERKVDLTSTACWTAAALVCLNTFIFIQ 300
Db 241 MLAYPFYLMASPKGKSHYHPDSDLFLPKERKVDLTSTACWTAAALVCLNTFIFIQ 300
QY 241 MLAYPFYLMASPKGKSHYHPDSDLFLPKERKVDLTSTACWTAAALVCLNTFIFIQ 300
Db 301 MLKLYGIPYWINVWMLDEVYTLHHGHEDKLPWYRGKEMSYLRGGLTLLDRDYGILNNIH 360
QY 301 MLKLYGIPYWINVWMLDEVYTLHHGHEDKLPWYRGKEMSYLRGGLTLLDRDYGILNNIH 360
Db 361 HDIGHVHNLHPOLPHYHLEATEAKPYLGKYRPPDKSGPLPHLETLAKSIXEDH 420
QY 361 HDIGHVHNLHPOLPHYHLEATEAKPYLGKYRPPDKSGPLPHLETLAKSIXEDH 420
Db 421 YVSDGEVYVYKADPNLYGEVYKVRAD 446
QY 421 YVSDGEVYVYKADPNLYGEVYKVRAD 446

RESULT 2
ID FD3C-BRANA STANDARD: PRT: 404 AA.
AC P48618;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-)
DE (FRAGMENT).
GN FAD7.
OS BRASSICA NAPUS (RAPE).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC

OC EUPHYLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAMPARALLES; BRASSICACEAE; BRASSICA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SEED:
RX MEDLINE: 94302147.
RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases."
RT PLANT PHYSIOL. 103:467-476(1993).
RL PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
DR EMBL: L22963; G408490; ALT_INIT.
DR PIR: P00812; P00812.
DR PFM: PF00487; FA.desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT NON_TER 1 1
FT TRANSIT 1 ?
FT CHAIN 1 ?
FT CHLOROPLAST (POTENTIAL).
FT OMEGA-3 FATTY ACID DESATURASE,
FT CHLOROPLAST.
FT DOMAIN 121 125 HISTIDINE BOX 1.
FT DOMAIN 157 161 HISTIDINE BOX 2.
FT DOMAIN 324 328 HISTIDINE BOX 3.
SQ SEQUENCE 404 AA; 46617 MW; 797F19FB CRC32;

Query Match 23.1%; Score 103; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 265 IPYWINVWMLDEVYTLHHGHEDKLPWYRGKEMSYLRGGLTLLDRDYGILNNIHHDIGTH 324
QY 307 IPYWINVWMLDEVYTLHHGHEDKLPWYRGKEMSYLRGGLTLLDRDYGILNNIHHDIGTH 366
Db 325 VINHLFPOIPIHYHLEATEAKPYLGKYRPPDKSGPLPHLL 367
QY 367 VINHLFPOIPIHYHLEATEAKPYLGKYRPPDKSGPLPHLL 409

RESULT 3
ID FD3C-RICCO STANDARD: PRT: 460 AA.
AC P48619;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7A-1.
OS RICINUS COMMUNIS (CASTOR BEAN).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC EUPHORBIALES; EUPHORBIACEAE; RICINUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. BAKER 296; TISSUE-SEED;

RX MEDLINE; 94302177.
CC VAN DE LOO F.J., SOMERVILLE C.R.;
RT "Plasmod omega-3 fatty acid desaturase cDNA from *Ricinus communis*."
RL PLANT PHYSIOL. 105:443-444(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL; L25897; G414732; -;
DR PFAM; PF00487; FA_desaturase; 1.
CC OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT CHAIN 1 460 CHLOROPLAST (POTENTIAL).
FT TRANSIT 1 460 OMEGA-3 FATTY ACID DESATURASE,
FT CHAIN ? 460 CHLOROPLAST.
FT DOMAIN 177 181 HISTIDINE BOX 1.
FT DOMAIN 213 217 HISTIDINE BOX 2.
FT DOMAIN 380 384 HISTIDINE BOX 3.
SQ SEQUENCE 460 AA; 52561 MW; DB3DA689 CRC32;

Query Match 9.9%; Score 44; DB 1; Length 460;
Best Local Similarity 100.0%; Pred. No. 5,10e-116;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 188 PKLNSVYGHLLHSSILVPHYHGRISHRTHQNHGVNDESMHP 231
OY 174 PKLNSVYGHLLHSSILVPHYHGRISHRTHQNHGVNDESMHP 217
|||||

RESULT 4
ID FD3C_ARATH STANDARD; PRT; 435 AA.
AC P48622;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
DE PRECURSOR (EC 1.14.99.-).
GN FAD8.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CARPRALES; BRASSICACEAE; ARABIDOPSIS.
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN-CV. COLUMBIA; TISSUE-AERIAL PARTS;
RA MEDLINE; 95148742.
RX GIBSON S., ARONDEL V., IBA K., SOMERVILLE C.R.;
RT "Cloning of a temperature-regulated gene encoding a chloroplast
RT omega-3 desaturase from *Arabidopsis thaliana*."
RL PLANT PHYSIOL. 106:1615-1621(1994).
RN [2]
CC SEQUENCE FROM N.A.
CC STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;
RA MATSUKI M.C., YAMAMOTO K.T.;
CC SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT

CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL; L27158; G516045; -;
DR EMBL; U08216; G497219; -;
DR EMBL; D17578; G471093; -;
CC OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT CHAIN 1 435 CHLOROPLAST (POTENTIAL).
FT TRANSIT 1 435 TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID
FT CHAIN ? 435 DESATURASE, CHLOROPLAST.
FT DOMAIN 156 160 HISTIDINE BOX 1.
FT DOMAIN 192 196 HISTIDINE BOX 2.
FT DOMAIN 359 363 HISTIDINE BOX 3.
SQ SEQUENCE 435 AA; 50136 MW; 70613FE0 CRC32;

Query Match 9.6%; Score 43; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,58e-112;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 INNTHDIGHVHHLPPQIPHYHLVATEAKVLYKYYREP 391
OY 356 INNTHDIGHVHHLPPQIPHYHLVATEAKVLYKYYREP 398
|||||

RESULT 5
ID FD3C_SESIN STANDARD; PRT; 447 AA.
AC P48620;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7.
OS SESAMUM INDICUM (ORIENTAL SESAME) (GINGELLY).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANANAE; LAMIALES; PEDALACEAE; SESAMUM.
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN-CV. 4294; TISSUE-COTYLEDON;
RA SHOU K.;
CC SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
DR EMBL: U25817; G870784; -
DR PRAM; PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT TRANSIT 1.
FT CHAIN ? 447 CHLOROPLAST (POTENTIAL).
FT FT ? 447 OMEGA-3 FATTY ACID DESATURASE,
FT DOMAIN 167 171 HISTIDINE BOX 1.
FT DOMAIN 203 207 HISTIDINE BOX 2.
FT DOMAIN 370 374 HISTIDINE BOX 3.
SQ SEQUENCE 447 AA; 5116 MM; 67B2C46B CRC32;

Query Match 8.1%; Score 36; DB 1; Length 447;
Best Local Similarity 100.0%; Prid. No. 2,56e-88;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 323 VTYLHHGHEDKLPYRGKEWSTYLGGLTTLDRODG 358
319 VTYLHHGHEDKLPYRGKEWSTYLGGLTTLDRODYG 354

RESULT 6 STANDARD; PROT; 453 AA.
ID ID PD3C SOYBN
AC PA8621; MEDLINE; 94302147.
RA YADAV N.S., WIERZBIICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHNEIDER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FEJDMANN K.A., PIERRE J., BROSE J.,
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLY).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
EMBL: L22965; GA08792; -.
DR PIR: JO2339; JO2339.
DR PRAM; PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT TRANSIT 1.
FT CHAIN ? 453 CHLOROPLAST (POTENTIAL).
FT FT ? 453 OMEGA-3 FATTY ACID DESATURASE,
FT DOMAIN 171 175 HISTIDINE BOX 1.
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FT DOMAIN 207 211 HISTIDINE BOX 2.
 FT DOMAIN 374 378 HISTIDINE BOX 3.
 SQ SEQUENCE 453 AA; 51362 MW; E4314F1B CRC32;

Query Match 8.18; Score 36; DB 1; Length 453;
 Best Local Similarity 100.0%; Pred. No. 2,55e-88;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 VTYLHHGHEDKLPWYRGKEMSYLRGLTTLDRDYG 362
 ||||||||||||||||||||||||||||||||||||||||
 QY 319 VTYLHHGHEDKLPWYRGKEMSYLRGLTTLDRDYG 354

RESULT 7
 ID FD31_BRANA STANDARD; PRT; 377 AA.
 AC P46311;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
 DE (VERSION 1).
 GN FAD3.
 OS BRASSICA NAPUS (RAPE).
 OC EMBRYOPHYTES: VIRIDIPHYTES: STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES: SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPPARALDES; BRASSICACEAE; BRASSICA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SEED;
 RX MEDLINE: 94302147.
 RA VADAV N.S., WIEZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ M.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL J.M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDAMANN K.A., PIERCE J.J., BROWSE J.;
 RT Cloning of higher plant omega-3 fatty acid desaturases. ;
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC
 DR EMBL; L22962; G408492; -
 DR PFAM; PF00487; FA_desaturase.1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 54 73 POTENTIAL.
 FT TRANSMEM 203 226 POTENTIAL.
 FT TRANSMEM 233 251 POTENTIAL.
 FT DOMAIN 92 96 HISTIDINE BOX 1.
 FT DOMAIN 128 132 HISTIDINE BOX 2.
 FT DOMAIN 295 299 HISTIDINE BOX 3.
 SQ SEQUENCE 377 AA; 43258 MW; 247237E0 CRC32;

Query Match 6.3%; Score 28; DB 1; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.55e-61;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

117 ILVYHGWRISHRTTHQNHGVENDESM 144


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OY 188 ILVPHGMRISHRTHONHGVENDESM 215
|||||
RESULT 8
ID FD32.BRANA STANDARD; PRT; 383 AA.
AC P48624;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (VERSION 2.).
GN FAD3.
OS BRASSICA NAPUS (RAPE);
OC EUKARYOTA: VIRIDIPANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC CAPRALES: BRASSICACEAE: BRASSICA.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 93088059.
RA ARONDEL V., LEMIEUX B., HWANG I., GIBSON S., GOODMAN H.M.,
RA SOMEVILLE C.R.;
RT "Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis.";
RL SCIENCE 258:1353-1355(1992).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC
CC EMBL: I01418; G167148; -
CC DR PFAM: PF00487; FA.desaturase: 1.
CC KX OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC KW TRANSMEMBRANE.
CC FT TRANSMEM 53 73 POTENTIAL.
CC FT TRANSMEM 210 230 POTENTIAL.
CC FT TRANSMEM 234 254 POTENTIAL.
CC FT DOMAIN 98 102 HISTIDINE BOX 1.
CC FT DOMAIN 134 138 HISTIDINE BOX 2.
CC FT DOMAIN 301 305 HISTIDINE BOX 3.
CC SQ SEQUENCE 383 AA; 43936 MW; F39A978B CRC32.

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Query Match 6.3%, Score 28; DB 1; Length 383;
 Best Local Similarity 100.0%; Pred. No. 2,356-61;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 123 ILVPHGMRISHRTHONHGVENDESM 150
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OY 188 ILVPHGMRISHRTHONHGVENDESM 215

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GN FAD3 OR F23F1.10.
OS AAABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA: VIRIDIPANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC CAPRALES: BRASSICACEAE: ARABIDOPSIS.
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN-CV. COLUMBIA; TISSUE-SEEDLING;
RX MEDLINE: 94302147.
RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRU L.,
RA KINNEY A.J., HITT W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
RN (2)
RP SEQUENCE FROM N.A.
RX STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;
RA WATAHAKI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN (3)
RP SEQUENCE FROM N.A.
RX STRAIN-CV. COLUMBIA;
RX MEDLINE: 94345020.
RA NISHIUCHI T., NISHIMURA M., ARONDEL V., IBA K.;
RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
RT fatty acid desaturase from Arabidopsis thaliana.";
RL PLANT PHYSIOL. 105:767-768(1994).
RN (4)
RP SEQUENCE FROM N.A.
RX STRAIN-CV. COLUMBIA;
RA ROUNDSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
RA SYKES S.M., KAIL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
RA SOMEVILLE C.R., VENTER J.C.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: MICROSOAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
CC DETECTABLE IN ROOT TISSUE.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC
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CC
CC EMBL: L22931; G408483; -
CC DR EMBL: D17579; G471091; -
CC DR EMBL: D26508; G1197795; -
CC DR EMBL: AC004680; G3420053; -
CC DR PFAM: PF00487; FA.desaturase: 1.
CC KX OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC KW TRANSMEMBRANE.
CC FT TRANSMEM 63 83 POTENTIAL.
CC FT TRANSMEM 220 240 POTENTIAL.
CC FT TRANSMEM 242 262 POTENTIAL.
CC FT DOMAIN 101 105 HISTIDINE BOX 1.
CC FT DOMAIN 137 141 HISTIDINE BOX 2.
CC FT DOMAIN 304 308 HISTIDINE BOX 3.
CC SQ SEQUENCE 386 AA; 44076 MW; C22B48BC CRC32.

```

Query Match 6.3%, Score 28; DB 1; Length 386;

Best Local Similarity 100.0%; Pred. No. 2,566-61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 ILVPGHGRISHRTHONHGHVDESN 153
|||||
QY 188 ILVPGHGRISHRTHONHGHVDESN 215

RESULT 10
ID FD3E-SOYBN STANDARD; PRT: 380 AA.
AC P48625;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
GN FAD3.
OS GLYCINE MAX (SOYBEAN).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RX MEDLINE: 94302147.
RA YADAV N.S., WIEZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRU L.,
RA KINNEA A.J., HITZ W.D., BOOTH J.R., SCHWETGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMANN K.A., PIERCE J., BROWSE J.;
RT Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: MICROSOAM (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTRAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL: L22964; G408794; -.
DR PIR: JQ2338; JQ2338.
DR PFAM: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 100 104 HISTIDINE BOX 1.
FT DOMAIN 136 140 HISTIDINE BOX 2.
FT DOMAIN 303 307 HISTIDINE BOX 3.
SQ SEQUENCE 380 AA; 44185 MW; E3C509B7 CRC32;

Query Match 6.1%; Score 27; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 5,186-51;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 295 NIHHDIGTHVHHLFPOIPHYHLEAT 321
|||||
QY 358 NIHHDIGTHVHHLFPOIPHYHLEAT 384

RESULT 11

ID EP3E-PHAAU STANDARD; PRT: 380 AA.
AC P32291;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
GN (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).
OS PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC FABALES; FABACEAE; PAPILIONOIDEAE; VIGNA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOCOTYL;
RA YAMAMOTO K.T., MORI H., IMASEKI H.;
RT Novel mRNA sequences induced by indole-3-acetic acid in sections of
RT elongating hypocotyls of mung bean (*Vigna radiata*).";
RL PLANT CELL PHYSIOL. 33:13-20(1992).
CC -1- FUNCTION: MICROSOAM (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTRAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL: D14410; G287562; -.
DR PIR: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 59 78 POTENTIAL.
FT TRANSMEM 208 231 POTENTIAL.
FT TRANSMEM 238 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
SQ SEQUENCE 380 AA; 43996 MW; 8429BF68 CRC32;

Query Match 5.6%; Score 25; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 1,866-51;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 294 NIHHDIGTHVHHLFPOIPHYHLEAT 318
|||||
QY 360 NIHHDIGTHVHHLFPOIPHYHLEAT 384

RESULT 12
ID FD3E-TOBAC STANDARD; PRT: 379 AA.
AC P48626;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
GN FAD3.
OS NICOTIANA TABACUM (COMMON TOBACCO).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANACEAE; SOLANACEAE; NICOTIANA.

[1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, SRL; TISSUE-LEAF;
RX MEDLINE; 95011632.
RA HANADA T., KODAMA H., NISHIMURA M., IBA K.;
RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";
RL GENE 147:293-294(1994).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.

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CC
DR EMBL; D26509; G599592; .
DR PFMAM; PF00487; FA-desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KM TRANSMEMBRANE.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 213 233 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
SQ SEQUENCE 379 AA; 44149 MW; C237E6D CRC32;

Query Match 5.4%; Score 24; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 3, 27e-48;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dc 291 NNHHDDIGTYHHLFPOIPHHL 314
|||
Qy 357 NNHHDDIGTYHHLFPOIPHHL 380

RESULT 13
ID RL1-TREPA STANDARD: PRT: 226 AA.
AC OR83266;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE 50S RIBOSOMAL PROTEIN L1.
GN RP1A OR TP0238.
GN TREPONEMA PALLIDUM.
OS BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; TREPONEMA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NICHOLS;
RX MEDLINE; 98332770.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DOOSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SOERGENSEN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCCONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL SCIENCE 281:375-388(1998).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS

```

CC LOCATED IN THE NEIGHBORHOOD OF THE SITE WHERE ELONGATION FACTOR TU
CC IS BOUND TO THE RIBOSOME (BY SIMILARITY).
CC
CC -1- SIMILARITY: BELONGS TO THE LIP FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL: AE001205; G3322508; -.
DR TIGR: TP0238; -.
DR PROSITE: PS01199; RIBOSOMAL_L1; 1.
RW RIBOSOMAL PROTEIN; RNA-BINDING.
SQ SEQUENCE 226 AA; 24977 MW; 423DBE8A1 CRC32;
Query Match 1.8%; Score 8; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 2,29e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 83 ALAAGAA 90
| | | | |
| 130 ALAAGAA 137
RESULT 14
ID KNIR DROME STANDARD; PRT; 429 AA.
AC P10734;
DT 01-JUL-1989 (REL. 11, CREATED)
DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ZYGOTIC GAP PROTEIN KNIRPS.
GN KNIR.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R; TISSUE-SALIVARY GLAND;
RX MEDLINE; 89057148.
RA NAUBER U., PANKRATZ M.J., KIHLIN A., SEYFERT E., KLEMM U.,
RA JACKLE H.;
RA "Abdominal segmentation of the Drosophila embryo requires a hormone
RT receptor-like protein encoded by the gap gene knirps.";
RT NATURE 336:489-492(1988).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE; 96312963.
RA ARNOST D.N., GRAY S., BAROLO S., ZHOU J., LEVINE M.;
RT "The gap protein knirps mediates both quenching and direct repression
in the Drosophila embryo.";
RL EMO J. 13:3659-3666(1996).
CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS TO MULTIPLE SITES IN
CC THE EYE STRIPE 3 ENHANCER ELEMENT. PLAYS AN ESSENTIAL ROLE IN THE
CC SEGMENTATION PROCESS BOTH BY REFINING THE EXPRESSION PATTERNS OF
CC GAP GENES AND BY ESTABLISHING PAIR-RULES STRIPES OF GENE
CC EXPRESSION.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC -----
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CC -----
DR EMBL: X13331; G6154; -.
DR PIR: S01919; S01919.

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DR FLYBASE: FBgn0001320; kni.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR PFAW: PF00105; ZF-C4; 1.
 DR HSSP: P03372; IHCO.
 DR TRANSFAC: T00445; "-
 KW RECEPTOR: TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
 KZ ZINC-FINGER: DEVELOPMENTAL PROTEIN; REPRESSOR.
 FT DNA_BIND 5 71 C4-TYPE ZINC FINGERS (TWO).
 FT ZN_FING 5 25 C4-TYPE.
 FT ZN_FING 42 66 C4-TYPE.
 FT DOMAIN 97 101 POLY-ALA.
 FT DOMAIN 137 142 POLY-HIS.
 FT DOMAIN 143 149 POLY-GLN.
 FT DOMAIN 200 213 POLY-ALA.
 FT DOMAIN 375 382 POLY-SER.
 SO SEQUENCE 429 AA; 45611 MW; 519CEDE CRC32;

Query Match 1.8%; Score 8; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 2.29e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 288 TSSSPLSF 295
 QY 43 TSSSPLSF 50

RESULT 15
 ID RL27_STRGR STANDARD; PRT; 85 AA.
 AC P95757;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE 50S RIBOSOMAL PROTEIN L27.
 GN RPMA.
 OS STREPTOMYCES GRISEUS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IFO 13189;
 RX MEDLINE; 97136618.
 RA OKAMOTO S., ITOH M., OCHI K.;
 RT "Molecular cloning and characterization of the obg gene of
 RT Streptomyces griseus in relation to the onset of morphological
 RT differentiation.";
 RL J. BACTERIOL. 179:170-179(1997).
 CC -! SIMILARITY: BELONGS TO THE L27P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL: D87916; GI783293; -
 DR PROSITE: PS00831; RIBOSOMAL_L27; 1.
 DR PFAW: PF01016; Ribosomal_L27; 1.
 KW RIBOSOMAL PROTEIN.
 SQ SEQUENCE 85 AA; 8860 MW; 804E9523 CRC32;

Query Match 1.6%; Score 7; DB 1; Length 85;
 Best Local Similarity 100.0%; Pred. No. 2.28e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 FALAAGA 66
 QY 129 FALAAGA 135

Search completed: Sat Aug 21 12:12:52 1999
 Job time : 49 secs.

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MPerch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:13:11 1999; Maspar time 25.58 Seconds

Tabular output not generated. 951.471 Million cell updates/sec

Title: >US-09-219-935-5
 Description: (1-446) from US0921935.pep
 Perfect Score: 446

Sequence: 1 MANVLVSECGIRPLRIYTT.....EVVYKADPNLYGEVYKVRAD 446

Scoring table: TABLE uninterpretable
 Gap 60

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

>sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 1:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 3.676; Variance 0.439; scale 8.391

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	47	10.5	436	Q40118	DELTA-15 LINCOLN DESAT	2,75e-121
2	43	9.6	398	Q24626	FATTY ACID DESATURASE	7,08e-108
3	40	9.0	431	Q82068	W-3 DESATURASE	6,87e-98
4	40	9.0	441	P93350	OMEGA-3 FATTY ACID DES	5,63e-88
5	37	8.3	438	Q04807	FATTY ACID DESATURASE	5,09e-84
6	36	8.1	443	Q23824	FATTY ACID DESATURASE	5,09e-84
7	34	7.6	438	P93452	OMEGA-3 FATTY ACID DES	5,36e-82
8	29	6.5	381	P94013	W-3 FATTY ACID DESATUR	5,36e-82
9	29	6.5	383	Q65792	OMEGA-3 FATTY ACID DES	5,36e-82
10	28	6.3	407	Q04907	OMEGA-3 DESATURASE (FR	8,26e-59
11	24	5.4	380	Q23802	PLASTID OMEGA-3 FATTY	3,10e-46
12	16	3.6	359	Q25240	DELTA-15 DESATURASE	2,51e-22
13	11	2.5	350	Q07872	OMEGA-3 DESATURASE	6,41e-09
14	9	2.0	494	Q17121	M15.1 PROTEIN	3,43e-04
15	8	1.8	193	Q07465	FATTY ACID DESATURASE	4,83e-02
16	8	1.8	445	Q23091	SIMILAR TO NADPH DEHYD	4,83e-02
17	8	1.8	598	Q44316	MALTOLOGOSYL TREHALOS	4,83e-02
18	8	1.8	1313	P87141	PUTATIVE GUANINE-NUCLE	4,83e-02
19	8	1.8	4848	Q07944	PRISTINAMYCIN I SYNTHA	4,83e-02
20	7	1.6	193	Q12064	D1554	4,40e+00

RESULT	ID	PRELIMINARY	PRT	436 AA
AC	Q40118			
DT	01-NOV-1996 (TREMBLREL, 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1999 (TREMBLREL, 09, LAST ANNOTATION UPDATE)			
DE	DELTA-15 LINCOLN DESATURASE			
OS	LIMNANTHES DOUGLASSII			
OC	EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:			
OC	EUPHYLLIOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:			
OC	CAPPARALES: LIMNANTHACEAE: LIMNANTHES			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE: 95334518			
RX	BHILLA R.S., MACKENZIE S.L.			
RT	"Nucleotide sequence of a cDNA from Limnantes douglasii L. encoding			
RT	a delta-15 linoleic acid desaturase."			
RL	PLANT PHYSIOL. 108:861-861(1995).			
DR	EMBL: U17063; G699390; -			
DR	PFAM: PF00487; FA_desaturase; 1.			
DR	MENDEL: 8699; LIMDO:1208;1.			
SO	SEQUENCE 436 AA; 50093 MW; 327D77FE CMC32;			

ALIGNMENTS

Query Match	10.5%	Score 47	DB 10	Length 436
Best Local Similarity 100.0%				
Matches 47; Conservative				
Mismatches 0; Indels 0; Gaps 0;				
DB 330 EWSYLRGGLTLDROYGLINNHHDTGYTHHLPDIPRYHLYEAT 376				
QY 338 EWSYLRGGLTLDROYGLINNHHDTGYTHHLPDIPRYHLYEAT 384				
RESULT 2				
AC Q24626; PRELIMINARY; PRT; 398 AA.				
DT 01-JAN-1998 (TREMBLREL, 05, CREATED)				
DT 01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)				
DT 01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)				
DE FATTY ACID DESATURASE (FRAGMENT).				
GN FAD8				
OS ZEA MAYS (MAIZE).				
OC EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:				
OC EUPHYLLIOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTA: LILIOPSIDA: POALES;				
OC POACEAE: ZEA.				

Query Match	8.1%	Score 36;	DB 10;	Length 443;
Best Local Similarity 100.0%;		Pred. No. 1.09e-84;		
Matches 36;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Db 317 VTLLHHGHEDKLPWYRGKEMSYLRGGITLTDRLDYG 352				
OY 319 VTLLHHGHEDKLPWYRGKEMSYLRGGITLTDRLDYG 354				
RESULT 7	PRELIMINARY;	PRT;	438 AA.	
AC P93452;				
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)				
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)				
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)				
DE OMEGA-3 FATTY ACID DESATURASE.				
DE PETROSELINUM CRISPUM (PARSLEY) (PETROSELINUM HORENSE).				
OC EUPHAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;				
OC EUPHYALOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;				
OC ASTERIDAE; ARALEALES; APICEAE; PETROSELINUM.				
RN [1]				
RP SEQUENCE FROM N.A.				
RA MEDLINE; 9720310.				
RX KIRSCH C., TAKAIWA-MIK M., REINOLD S., HAHNLOCK K., SOMSSICH I.E.;				
RT "Rapid, transient, and highly localized induction of plastidial				
RT peteoa3 fatty acid desaturase mRNA at fungal infection sites in				
RL PROC. NATL. ACAD. SCI. U.S.A. 94:2079-2084(1997).				
DR EMBL; U75745; G1786066; -				
DR PFMEL; PF00487; FA.desaturase; 1.				
DR MENDEL; 9788; PETCR:1208.1.				
SO SEQUENCE 438 AA; 50391 MW; 9E77A228 CRC32;				
Query Match	7.6%;	Score 34;	DB 10;	Length 438;
Best Local Similarity 100.0%;		Pred. No. 3.80e-78;		
Matches 34;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Db 180 LHSILVPHGMRISHRTHQNHGVNDESMWP 213				
OY 184 LHSILVPHGMRISHRTHQNHGVNDESMWP 217				
RESULT 8	PRELIMINARY;	PRT;	381 AA.	
ID P94013;				
AC P94013;				
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)				
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)				
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)				
DE W-3 FATTY ACID DESATURASE.				
DE ORYZA SATIVA (RICE).				
OC EUPHAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;				
OC EUPHYALOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOSSIDA; POALES;				
OC POACEAE; ORYZA.				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN-IR36, AND NIPPONBARE;				
RA AKAGI H.;				
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.				
DR EMBL; D78506; G177376; -				
DR EMBL; D78505; G1785856; -				
DR MENDEL; 9612; ORYSA:1208.1.				
SO SEQUENCE 381 AA; 43640 MW; 2BD4ED6E CRC32;				
Query Match	6.5%;	Score 29;	DB 10;	Length 381;
Best Local Similarity 100.0%;		Pred. No. 5.36e-67;		
Matches 29;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Db 288 INNHHDIGTVIHNLFPQIPHYHLVEAT 316				
OY 356 INNHHDIGTVIHNLFPQIPHYHLVEAT 384				

ID	065792	PRELIMINARY;	PT:	383 AA.
AC	065792	PRELIMINARY;	PT:	383 AA.
DT	01-AUG-1998	(TREMBLREL. 07, CREATED)		
DT	01-AUG-1998	(TREMBLREL. 07, LAST SEQUENCE UPDATE)		
DT	01-AUG-1998	(TREMBLREL. 07, LAST ANNOTATION UPDATE)		
DE	OMEGA-3 FATTY ACID DESATURASE.			
GN	TANAD3.			
OS	TRITICUM AESTIVUM (WHEAT).			
OC	EDUARVOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;			
OC	EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;			
OC	POACEAE; TRITICUM.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CV, CHIHOKU; TISSUE-LEAF, AND ROOT.			
RA	HORIGUCHI G., KAWAKAMI N., KUSUMI K., KODAMA H., IBA K.;			
RL	PLANT CELL PHYSIOL. 39:540-544(1998).			
DR	EMBL; D84678; D1029298; -			
SO	SEQUENCE 383 AA; 43687 MW; 50D38F40 CRC32;			
Query Match 6.5%; Score 29; DB 10; Length 383;				
Best Local Similarity 100.0%; Pred. No. 5,36e-62;				
Matches 29; Conservative 0; Mismatches 0; Gaps 0;				
Dy	290	NNIHHDIGTVIHHLFPOIPHYHLEAT 318		
Qy	356	NNIHHDIGTVIHHLFPOIPHYHLEAT 384		
RESULT 10				
ID	064907	PRELIMINARY;	PT:	407 AA.
AC	064907	PRELIMINARY;	PT:	407 AA.
DT	01-AUG-1998	(TREMBLREL. 07, CREATED)		
DT	01-AUG-1998	(TREMBLREL. 07, LAST SEQUENCE UPDATE)		
DT	01-AUG-1998	(TREMBLREL. 07, LAST ANNOTATION UPDATE)		
DE	OMEGA-3 DESATURASE (FRAGMENT).			
GN	PMX-15.			
OS	PEARLCONIUM X HORTORUM.			
OC	EDUARVOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;			
OC	EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;			
OC	GERANIALES; GERANIACEAE; PEARLCONIUM.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	SCHULTZ D.J., MONMA R.O., COX-FOSTER D., CRAIG R., MEDFORD J.I.;			
RL	SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL; AF020204; G3133289; -			
FT	NON TER 1			
SO	SEQUENCE 407 AA; 47169 MW; BC150974 CRC32;			
Query Match 6.3%; Score 28; DB 10; Length 407;				
Best Local Similarity 100.0%; Pred. No. 8,26e-59;				
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Dy	318	NNIHHDIGTVIHHLFPOIPHYHLEAT 345		
Qy	357	NNIHHDIGTVIHHLFPOIPHYHLEAT 384		
RESULT 11				
ID	023802	PRELIMINARY;	PT:	380 AA.
AC	023802	PRELIMINARY;	PT:	380 AA.
DT	01-JAN-1998	(TREMBLREL. 05, CREATED)		
DT	01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)		
DE	PLASTID OMEGA-3 FATTY ACID DESATURASE (FRAGMENT).			
GN	TANAD7.			
OS	TRITICUM AESTIVUM (WHEAT).			
OC	EDUARVOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;			
OC	EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;			
OC	POACEAE; TRITICUM.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CV, CHIHOKU; TISSUE-LEAF;			
RA	HORIGUCHI G., IWAKAWA H., KODAMA H., KAWAKAMI N., NISHIMURA M.;			

RA IBA K.;
RL PHYSTOL. PLANTARUM 96:275-283(1996).
DR EMBL: D43688; D1008371; -.
DR PFAM: PF00487; FA_desaturase; 1.
FT NON-TER
SQ SEQUENCE 380 AA; 42633 MW; 2123FF56 CRC32;
Query Match 5.4%; Score 24; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.10e-46;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 130 GWRISHRTHONGHVENDESNHP 153
QY 194 GWRISHRTHONGHVENDESNHP 217
RESULT 12
ID 055240; PRELIMINARY; PRT; 359 AA.
AC 055240;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE DELTA 15 DESATURASE.
GN DESB.
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95035996.
RA SAKAMOTO T., LOS D.A., HIGASHI S., WADA H., NISHIDA I., OHMORI M.,
RA MURATA N.;
RT "Cloning of omega 3 desaturase from cyanobacteria and its use in
RT altering the degree of membrane lipid unsaturation.";
RL PLANT MOL. BIOL. 26:249-263(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA TABATA S.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97061201.
RA KANKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARDO K., OKUMURA S.,
RA SHIMO S., TAEDECHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
RA TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA RES. 3:109-116(1996).
DR EMBL: D13780; G600598; -.
DR PFAM: D90913; G1653388; -.
DR PFAM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 359 AA; 41919 MW; B5375D98 CRC32;
Query Match 3.6%; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.51e-22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 114 ILVPHGWRISHRTH 129
QY 188 ILVPHGWRISHRTH 203
RESULT 13
ID 007872; PRELIMINARY; PRT; 350 AA.
AC 007872;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE OMEGA-3 DESATURASE.
GN DESB.
OS SYNECHOCOCUS PCC7002.

OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCOCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97260123.
RA SAKAMOTO T., BRYANT D.A.;
RT "Temperature-regulated mRNA accumulation and stabilization for fatty
RT acid desaturase genes in the cyanobacterium Synechococcus sp. strain
RT PCC 7002.";
RL MOL. MICROBIOL. 23:1281-1292(1997).
DR EMBL: U36389; G2197199; -.
DR PFAM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 350 AA; 40562 MW; 969CAD61 CRC32;
Query Match 2.5%; Score 11; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.41e-09;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 74 AOGTFMFLFY 84
QY 150 AOGTFMFLFY 160
RESULT 14
ID 017121; PRELIMINARY; PRT; 494 AA.
AC 017121;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE M151.1 PROTEIN.
GN M151.1.
OS CAENORHABDITIS ELEGANS.
OC EUDAROTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA GRAYTON M., DEAR S., DU Z., DURBIN R., FAYELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIR M., JOHNSTON L.,
RA JONES M., KESHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHNING J., LOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPRAT J., WOHIDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA GARTUNG S., GOELA D.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF024502; G2394495; -.
SQ SEQUENCE 494 AA; 57632 MW; 186202ED CRC32;
Query Match 2.0%; Score 9; DB 5; Length 494;
Best Local Similarity 100.0%; Pred. No. 3.43e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 295 SSSSYKTS 303
QY 37 SSSSYKTS 45
RESULT 15

ID 074645 PRELIMINARY; PRT: 193 AA.
AC 074645;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
OS GIBBERELLA ZEAE.
OS EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
OC HYPOCREALES; HYPOCREACEAE; GIBBERELLA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-F15;
RX MEDLINE; 98433864.
RA KIMURA M., MATSUMOTO G., SHINGU Y., YONEYAMA K., YAMAGUCHI I.;
RT "The mystery of the trichothecene 3-O-acetyltransferase gene.
RT Analysis of the region around Trl101 and characterization of its
RT homologue from Fusarium sporotrichioides.";
RL FEBS LETT. 435:163-168(1998).
DR EMBL; AB014492; D1034743; -.
FT NON_TER 1
FT NON_TER 193
SO SEQUENCE 193 AA; 21845 MW; BF2053ED CRC32;

Query Match 1.8%; Score 8; DB 3; Length 193;
Best Local Similarity 100.0%; Pred.No. 4.83e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 186 HVTHLFP 193
OY 366 HVTHLFP 373

Search completed: Sat Aug 21 12:15:00 1999
Job time : 109 secs.

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QY 121 VVRDVAIVFALAAAGAAIYNMIVWPLYLWLAOGTFMFLFVGHDCGHSFSDPKLSNV 180
D 181 GHLLHSSILVYHGWISHTRHQNHGHVENDSWHMPSEKIYNTLDKPTFFFTPLV 240
QY 181 GHLLHSSILVYHGWISHTRHQNHGHVENDSWHMPSEKIYNTLDKPTFFFTPLV 240
D 241 MLYAPFYIWAESPQKSGSHYHPDSDLFPERKRDVLSTACWTMAALLVCLNFTIGPIQ 300
QY 241 MLYAPFYIWAESPQKSGSHYHPDSDLFPERKRDVLSTACWTMAALLVCLNFTIGPIQ 300
D 301 MLKLYGIPYWINVMWLDFTVYLHHGHEDKLPYRGKESYLIGLITLTDYGLINIH 360
QY 301 MLKLYGIPYWINVMWLDFTVYLHHGHEDKLPYRGKESYLIGLITLTDYGLINIH 360
D 361 HDIGTHVHNHLPQIPHYHLVEATEAKPVLGKYYREPKSGPLPHLEILAKSIKEDH 420
QY 361 HDIGTHVHNHLPQIPHYHLVEATEAKPVLGKYYREPKSGPLPHLEILAKSIKEDH 420
D 421 YVSDGEVYVYKADPNLYGEVKVRAD 446
QY 421 YVSDGEVYVYKADPNLYGEVKVRAD 446
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RESULT 2
ID R37593 standard; Protein; 446 AA.
AC R37593;
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone PACF2-2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO ) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
PI WPI; 93-197063/24.
DR N-PSDB; Q43204.
PT Isolated nucleic acid fragment, for plant lipid compen.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 132-134; 167pp; English.
PC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. In contrast to the
CC constitutive expression of the gene encoding (R37592), the mRNA
CC corresponding to Q43204 is abundant in green tissues, rare in roots
CC and leaves, and is about three-fold more abundant in leaf than that
CC of Q43202. R37592 and R37593 show overall homology of approx.
CC 80%.
SQ Sequence 446 AA;
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Query Match 100.0%; Score 446; DB 7; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
D 1 MANLVLSGCGIRPLRITTPRSNLFNNKFRPSLSSSSKTISSPISFGINSDDGTR 60
QY 1 MANLVLSGCGIRPLRITTPRSNLFNNKFRPSLSSSSKTISSPISFGINSDDGTR 60
D 61 NVALNVSPLTPIFEESPLEEDNKGKRFDPGAPPPFNADIRAIKPKCWNKPKKSLSY 120
QY 61 NVALNVSPLTPIFEESPLEEDNKGKRFDPGAPPPFNADIRAIKPKCWNKPKKSLSY 120
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D 121 VVRDVAIVFALAAAGAAIYNMIVWPLYLWLAOGTFMFLFVGHDCGHSFSDPKLSNV 180
QY 121 VVRDVAIVFALAAAGAAIYNMIVWPLYLWLAOGTFMFLFVGHDCGHSFSDPKLSNV 180
D 181 GHLLHSSILVYHGWISHTRHQNHGHVENDSWHMPSEKIYNTLDKPTFFFTPLV 240
QY 181 GHLLHSSILVYHGWISHTRHQNHGHVENDSWHMPSEKIYNTLDKPTFFFTPLV 240
D 241 MLYAPFYIWAESPQKSGSHYHPDSDLFPERKRDVLSTACWTMAALLVCLNFTIGPIQ 300
QY 241 MLYAPFYIWAESPQKSGSHYHPDSDLFPERKRDVLSTACWTMAALLVCLNFTIGPIQ 300
D 301 MLKLYGIPYWINVMWLDFTVYLHHGHEDKLPYRGKESYLIGLITLTDYGLINIH 360
QY 301 MLKLYGIPYWINVMWLDFTVYLHHGHEDKLPYRGKESYLIGLITLTDYGLINIH 360
D 361 HDIGTHVHNHLPQIPHYHLVEATEAKPVLGKYYREPKSGPLPHLEILAKSIKEDH 420
QY 361 HDIGTHVHNHLPQIPHYHLVEATEAKPVLGKYYREPKSGPLPHLEILAKSIKEDH 420
D 421 YVSDGEVYVYKADPNLYGEVKVRAD 446
QY 421 YVSDGEVYVYKADPNLYGEVKVRAD 446
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RESULT 3
ID R37591 standard; Protein; 378 AA.
AC R37591;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone PBNSF3-f2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO ) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
PI WPI; 93-197063/24.
DR N-PSDB; Q43205.
PT Isolated nucleic acid fragment, for plant lipid compen.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 136-138; 167pp; English.
PC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from PCF3 and PCM2 were used to isolate PBNSF3-2. Plasmid PBNSF3-2
CC was deposited as ATCC No. 68854. PBNSF3-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 378 AA;
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Query Match 23.1%; Score 103; DB 7; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.98e-162;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
D 239 IPYWINVMWLDFTVYLHHGHEDKLPYRGKESYLIGLITLTDYGLINIHIDGTH 298
QY 307 IPYWINVMWLDFTVYLHHGHEDKLPYRGKESYLIGLITLTDYGLINIHIDGTH 366
D 299 VVHNLFPQIPHYHLVEATEAKPVLGKYYREPKSGPLPHLHL 409
QY 367 VVHNLFPQIPHYHLVEATEAKPVLGKYYREPKSGPLPHLHL 409
```

RESULT 4
ID R37594 standard; Protein; 404 AA.
AC R37594;
DT 01-OCT-1993 (first entry)
DE Sequence of plastid delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone PBNSFd-2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPLO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR N-PSDB; 043306.
PT Isolated nucleic acid fragment, for plant lipid compn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 140-141; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from PCF3 and PCM2 were used to isolate PBNSF3-2. Plasmid PBNSF3-2
CC was deposited as ATCC No. 68854. PBNSFd-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 404 AA:

Query Match 23.1%; Score 103; DB 7; Length 404;
Best Local Similarity 100.0%; Pred. No. 2,98e-162;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 265 lpyvlnvwmldfvtyllhghghedklpwrgkewylrglgtltdygltnlthdylgch 324
|||||
QY 307 lpyvlnvwmldfvtyllhghghedklpwrgkewylrglgtltdygltnlthdylgch 366
|||||
QY 367 vihlhfpqirhyhlveateakpvlgykyrepdksqplrhll 367
|||||
QY 367 vihlhfpqirhyhlveateakpvlgykyrepdksqplrhll 409
|||||

RESULT 5
ID R60500 standard; Protein; 435 AA.
AC R60500;
DT 28-MAR-1995 (first entry)
DE linoletic-acid-desaturase fade.
KW linoletic-acid-desaturase; fade; transgenic plant; crop improvement;
OS linoletic acid.
OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PI (UNMS) UNITV MICHIGAN STATE.
PI Atondel VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
DR WPI; 94-279758/34.
DR N-PSDB; Q71211.
PT Genetically transformed plants with altered linoletic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoletic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure: Page 79-81; 144pp; English.

CC The cDNA sequence and deduced amino acid sequence of linoletic-
CC acid-desaturase fade of Arabidopsis are provided.
SQ Sequence 435 AA;

Query Match 9.6%; Score 43; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.59e-56;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 lnnlhhdgchvhlhfpqirhyhlveateakpvlgykyrep 391
|||||
QY 356 lnnlhhdgchvhlhfpqirhyhlveateakpvlgykyrep 398
|||||

RESULT 6
ID W13381 standard; Protein; 447 AA.
AC W13381;
DT 02-DEC-1997 (first entry)
DE Sesame omega-3 alphabetic acid desaturase.
KW Sesame; omega-3 alphabetic acid desaturase; modify; fat; oil; plant;
KW linoletic acid; recombinant production.
OS Sesamum indicum.
PN J0905882-A.
PD 11-MAR-1997.
PF 01-SEP-1995; 225145.
PR 01-SEP-1995; JP-225145.
PA (TOYA-) TOYAMA KEN.
DR WPI; 97-220417/20.
DR N-PSDB; T62065.
PT Sesame omega-3 alphabetic acid desaturase gene - useful in genetic
PT engineering to modify fats and oils in agricultural products
PS Claim 6; Page 4; 10pp; Japanese.
CC This protein is a sesame omega-3 alphabetic acid desaturase. Its coding
CC sequence can be used in genetic engineering to modify fats and oils in
CC agricultural products. The gene or enzyme can be introduced into a plant
CC to modify the alphabetic acid composition in its oils and fats, to give
CC oils and fats with a high content of linoletic acid. Antisense DNA can
CC be introduced into a plant to inhibit the expression of the gene, so
CC that oils and fats with little or no linoletic acid are produced. The
CC gene can also be expressed in microorganisms for recombinant production
CC the enzyme.
SQ Sequence 447 AA:

Query Match 8.1%; Score 36; DB 24; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.46e-44;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 323 vtyllhghghedklpwrgkewylrglgtltdygltnlthdylgch 358
|||||
QY 319 vtyllhghghedklpwrgkewylrglgtltdygltnlthdylgch 354
|||||

RESULT 7
ID R37596 standard; Protein; 453 AA.
AC R37596;
DT 01-OCT-1993 (first entry)
DE Sequence of soybean plastid delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pSPD-118bp.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPLO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; Q43208.
PT Isolated nucleic acid fragment, for plant lipid compn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS PCF3 was isolated from a cDNA library using a 5.2 kb Hind III

CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15
 CC desaturase cDNA was used as a hybridization probe to isolate a
 CC glycerolipid desaturase cDNA from soybean. Plasmid pXFI was
 CC deposited under ATCC 68874. Soybean microsomal delta-15
 CC desaturase cDNA was used as a hybridization probe to isolate cDNAs
 CC encoding related desaturases from soybean. The insert of
 CC pSPD-118bp contained a stretch of 1675 nucleotides which contained
 CC an open-reading frame encoding a polypeptide (R37596) of about
 CC 80k identity with, and colinear with, the Arabidopsis plastid
 CC delta-15 desaturase polypeptide listed in R37593. Nucleotides 169
 CC to 382 encode the putative plastid transit peptide, colinear with
 CC and sharing some homology with the transit peptide described for
 CC the Arabidopsis plastid delta-15 glycerolipid desaturase (R37593).
 SQ Sequence 453 AA;

Query Match 8.1%; Score 36; DB 7; Length 453;

Best Local Similarity 100.0%; Pred. No. 1,46e-44; Mismatches 0; Indels 0; Gaps 0;

Db 327 vtylhhghedklpwyrgkewylrgltldrdyg 362
 QY 319 VTYLHHGHEDKLPMWRGKMSYLRGLTLDRDYG 354

RESULT 8
 ID R37598 standard; Protein; 156 AA.
 AC R37598;
 DT 01-OCT-1993 (first entry)
 DE Sequence of a plastid delta-15 fatty acid.
 KW Lipid composition; modification; fatty acid desaturase; enzyme.
 OS Arabidopsis thaliana, clone pRadx-2 and pRadcp7.
 PN W09311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: Q43210.
 PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure; Page 155; 167pp; English.
 PC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. Q43210 is the partial
 CC composite sequence derived from the inserts in plasmids pRadx-2 and
 CC pRadcp7. R37598 is a deduced partial peptide sequence of its ORF.
 SQ Sequence 156 AA;

Query Match 6.5%; Score 29; DB 7; Length 156;

Best Local Similarity 100.0%; Pred. No. 8,60e-33; Mismatches 0; Indels 0; Gaps 0;

Db 32 rfdpappfnnladiiraaiiphkwknpw 60
 QY 87 RFDGAPPFPFNLDIRAIIPKHCWKWKNPM 115

RESULT 9
 ID R60498 standard; Protein; 383 AA.
 AC R60498;
 DT 28-MAR-1995 (first entry)
 DE Linoleic-acid-desaturase fad3
 KW Linoleic-acid-desaturase; fad3; oilseed rape; rapeseed;
 KW transgenic plant; crop improvement; yeast artificial chromosome;
 KW YAC; linoleic acid.
 OS Brassica napus.
 PN W09418337-A.
 PD 18-AUG-1994.
 PF 04-FEB-1994; U01321.
 PR 05-FEB-1993; US-014431.
 PR 22-NOV-1993; US-156551.
 PA (MONS) MONSANTO CO.
 PA (UNMS) UNIV MICHIGAN STATE.
 PI Aronow V, Gibson SJ, Kishore GM, Ruff TG, Somerville CR;
 DR WPI: 94-279758/34.
 DR N-PSDB: Q71203.
 PT Genetically transformed plants with altered linoleic acid
 PT content - contg recombinant, double-stranded DNA encoding
 PT linoleic acid desaturase, or the antisense of the coding
 PT sequence
 PS Disclosure; Page 69-71; 144pp; English.
 CC cDNA encoding the linoleic-acid-desaturase (fad3) of B. napus was
 CC isolated from a YAC library using RFLP 220 and ASA2 markers as
 CC probes. Isolated DNA was amplified using the primers given in
 CC Q71204-09, and used to screen YAC libraries. The fad3 gene was
 CC identified in YAC EW7D11.
 SQ Sequence 383 AA;

Query Match 6.3%; Score 28; DB 11; Length 383;

Best Local Similarity 100.0%; Pred. No. 3,94e-31; Mismatches 0; Indels 0; Gaps 0;

Db 123 ilvpyghytrshrhqnhghvdesw 150
 QY 188 ILVPGHWRISHRTHQNHGHVDESM 215

RESULT 10
 ID R37592 standard; Protein; 386 AA.
 AC R37592;
 DT 01-OCT-1993 (first entry)
 DE Sequence of delta-15 desaturase.
 KW Lipid composition; modification; fatty acid desaturase; enzyme.
 OS Arabidopsis thaliana, clone pCF3.
 PN W09311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: Q43202.
 PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure; Page 127-129; 167pp; English.
 PC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224.
 SQ Sequence 386 AA;

DT 19-JAN-1996 (first entry)
DE Trehalose releasing enzyme.
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriose; alpha-maltotetraose; alpha-maltopentaose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
OS Archaeobacter sp. Q36.
PN EP-671470-A2.
PD 13-SEP-1995.
PE 07-MAR-1995: 301474.
PR 07-MAR-1994: JP-059840.
PR 07-MAR-1994: JP-059834.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
DR WPI: 95-312772/41.
DR N-PSDB: Q98670.
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
PT from a non-reducing saccharide having a trehalose structure as an
PT end unit.
PS Claim 3; Page 24-25; 45pp; English.
CC This enzyme can be used for the preparation of trehalose with high
CC yields and efficiency from non-reducing saccharides such as
CC alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriose, alpha-maltotetraose and
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
SQ Sequence 597 AA;

Query Match 1.8%; Score 8; DB 14; Length 597;
Best Local Similarity 100.0%; Pred. No. 1.46e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 eaakpvlg 14
|||||||
QY 385 ERAKPVLG 392

RESULT 15
ID R77471 standard; Protein; 598 AA.
AC R77471.
DT 25-JAN-1996 (first entry)
DE Trehalose releasing enzyme.
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriose; alpha-maltotetraose; alpha-maltopentaose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
OS Archaeobacter sp. Q36.
PN EP-671470-A2.
PD 13-SEP-1995.
PE 07-MAR-1995: 301474.
PR 07-MAR-1994: JP-059840.
PR 07-MAR-1994: JP-059834.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
DR WPI: 95-312772/41.
DR N-PSDB: Q98672.
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
PT from a non-reducing saccharide having a trehalose structure as an
PT end unit.
PS Claim 6; Page 27-29; 45pp; English.
CC This enzyme can be used for the preparation of trehalose with high
CC yields and efficiency from non-reducing saccharides such as
CC alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriose, alpha-maltotetraose and
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
SQ Sequence 598 AA;

Query Match 1.8%; Score 8; DB 14; Length 598;

Best Local Similarity 100.0%; Pred. No. 1.46e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 8 eaakpvlg 15
|||||||
QY 385 ERAKPVLG 392

Search completed: Sat Aug 21 12:10:19 1999
Job time : 222 secs.

Db 267 YWVWMLDEVYTLHHGHEDKLPWYRGKEMSYLRGSLTTLDRDYGILNNIHHDIGTHVI 326
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QY 241 YWVWMLDEVYTLHHGHEDKLPWYRGKEMSYLRGSLTTLDRDYGILNNIHHDIGTHVI 300
|||||
Db 327 HHLPPOIPHYHLVLEATEAKPVLGKYYRPPDKSGPLPLHLGLIAKSKEDEHFPVSDGDV 386
|||||
QY 301 HHLPPOIPHYHLVLEATEAKPVLGKYYRPPDKSGPLPLHLGLIAKSKEDEHFPVSDGDV 360
|||||
Db 387 VYVADPNLYGEIKVTAE 404
|||||
QY 361 VYVADPNLYGEIKVTAE 378
|||||
RESULT 2
ENTRY JQ2336 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CFD -
ORGANISM Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
#accession JQ2336
#cross-references EMBL:D63953; NID:d116445; PID:d1023305
#experimental_source strain honey bantum
GENETICS
#gene FAD8
#keywords oxidoreductase
SUMMARY #length 398 #checksum 5580
Query Match 11.4%; Score 43; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.62e-102;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 291 EWSYLRGSLTTLDRDYGILNNIHHDIGTHVIHHLFPOIPHYHL 333
|||||
QY 270 EWSYLRGSLTTLDRDYGILNNIHHDIGTHVIHHLFPOIPHYHL 312
|||||
RESULT 4
ENTRY T03029 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - common
ORGANISM tobacco
#formal_name Nicotiana tabacum #common_name common tobacco
DATE 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
ACCESSION T03029
REFERENCE Z1828
#authors Hamada, T.; Nishituchi, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Plant Cell Physiol. (1996) 37:606-611
#title CDNA cloning of a wounding-inducible gene encoding a plastid
omega-3 fatty acid desaturase from tobacco.
#accession T03029
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-441 #label HAM
#cross-references EMBL:D79979; NID:d1093316; PID:g1694625
#experimental_source cultivar SRI
GENETICS
#gene FAD7
#keywords superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 441 #molecular_weight 50310 #checksum 6941
Query Match 10.6%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.29e-93;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 355 INNHHDIGTHVIHHLFPOIPHYHLVLEATEAKPVLGKYY 394
|||||
QY 288 INNHHDIGTHVIHHLFPOIPHYHLVLEATEAKPVLGKYY 327
|||||
RESULT 5
ENTRY T01697 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize
ORGANISM #formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 19-Feb-1999

Db 267 YWVWMLDEVYTLHHGHEDKLPWYRGKEMSYLRGSLTTLDRDYGILNNIHHDIGTHVI 326
|||||
QY 241 YWVWMLDEVYTLHHGHEDKLPWYRGKEMSYLRGSLTTLDRDYGILNNIHHDIGTHVI 300
|||||
Db 327 HHLPPOIPHYHLVLEATEAKPVLGKYYRPPDKSGPLPLHLGLIAKSKEDEHFPVSDGDV 386
|||||
QY 301 HHLPPOIPHYHLVLEATEAKPVLGKYYRPPDKSGPLPLHLGLIAKSKEDEHFPVSDGDV 360
|||||
Db 387 VYVADPNLYGEIKVTAE 404
|||||
QY 361 VYVADPNLYGEIKVTAE 378
|||||
RESULT 2
ENTRY JQ2336 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CFD -
ORGANISM Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
#accession JQ2336
#cross-references EMBL:D63953; NID:d116445; PID:d1023305
#experimental_source strain honey bantum
GENETICS
#gene FAD8
#keywords oxidoreductase
SUMMARY #length 398 #checksum 5580
Query Match 11.4%; Score 43; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.62e-102;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 291 EWSYLRGSLTTLDRDYGILNNIHHDIGTHVIHHLFPOIPHYHL 333
|||||
QY 270 EWSYLRGSLTTLDRDYGILNNIHHDIGTHVIHHLFPOIPHYHL 312
|||||
RESULT 4
ENTRY T03029 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - common
ORGANISM tobacco
#formal_name Nicotiana tabacum #common_name common tobacco
DATE 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
ACCESSION T03029
REFERENCE Z1828
#authors Hamada, T.; Nishituchi, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Plant Cell Physiol. (1996) 37:606-611
#title CDNA cloning of a wounding-inducible gene encoding a plastid
omega-3 fatty acid desaturase from tobacco.
#accession T03029
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-441 #label HAM
#cross-references EMBL:D79979; NID:d1093316; PID:g1694625
#experimental_source cultivar SRI
GENETICS
#gene FAD7
#keywords superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 441 #molecular_weight 50310 #checksum 6941
Query Match 10.6%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.29e-93;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 355 INNHHDIGTHVIHHLFPOIPHYHLVLEATEAKPVLGKYY 394
|||||
QY 288 INNHHDIGTHVIHHLFPOIPHYHLVLEATEAKPVLGKYY 327
|||||
RESULT 5
ENTRY T01697 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize
ORGANISM #formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 19-Feb-1999

ACCESSIONS T01697
REFERENCE Z14400
#authors Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.; Kusano, T.
#journal Plant Mol. Biol. (1998) 36:297-306
#title Two maize genes encoding omega-3 fatty acid desaturase and their differential expression to temperature.
#accession T01697
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-443 #label BBR
##cross-references EMBL:D63954; NID:d1164453; PID:d1023306
#experimental_source strain honey bantam

GENETICS
#gene FAD7
#introns 163/2: 193/2: 215/3: 246/3: 308/3: 335/3: 381/3
KEYWORDS oxidoreductase
SUMMARY #length 443 #molecular-weight 49437 #checksum 8872

Query Match 9.5%; Score 36; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 2,236-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 317 VTYLHHGHEDKLPYRGKESYLRGGLTTLDRDYG 352
QY 251 VTYLHHGHEDKLPYRGKESYLRGGLTTLDRDYG 286

RESULT 6
ENTRY JQ2339
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

ACCESSIONS JQ2339
REFERENCE JQ2335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:GMD
#accession JQ2339
##molecule_type mRNA
##status Preliminary; not compared with conceptual translation
##residues 1-453 #label YAD
##cross-references GB:I22965; NID:9408791; PID:9408792
COMMENT This enzyme introduces the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 453 #molecular-weight 51362 #checksum 7549

Query Match 9.5%; Score 36; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 2,236-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 VTYLHHGHEDKLPYRGKESYLRGGLTTLDRDYG 362
QY 251 VTYLHHGHEDKLPYRGKESYLRGGLTTLDRDYG 286

RESULT 7
ENTRY JQ2337
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BNS - rape
ORGANISM #formal_name Brassica napus #common_name rape
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

ACCESSIONS JQ2337
REFERENCE JQ2335

#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:BNS
#accession JQ2337
##molecule_type mRNA
##status Preliminary; not compared with conceptual translation
##residues 1-377 #label YAD
##cross-references GB:I22962; NID:9408491; PID:9408492
COMMENT This enzyme introduces the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 377 #molecular-weight 43258 #checksum 3294

Query Match 7.4%; Score 28; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 6,876-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 117 ILVPHGWRISHRTHQNHGVNDESM 144
QY 120 ILVPHGWRISHRTHQNHGVNDESM 147

RESULT 8
ENTRY A44227
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - rape
ALTERNATE_NAMES omega-3 linoleate desaturase
ORGANISM #formal_name Brassica napus #common_name rape
DATE 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

ACCESSIONS A44227
REFERENCE A44227
#authors Aronold, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman, H.M.; Somerville, C.R.
#journal Science (1992) 258:1353-1355
#title Map-based cloning of a gene controlling omega-3 fatty acid desaturation in Arabidopsis.
#cross-references MUID:93088059
#accession A44227
##status Preliminary; not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-383 #label ARO
##cross-references GB:I01418; NID:9167147; PID:9167148
##experimental_source developing seed
COMMENT Sequence extracted from NCBI backbone (NCBIP:119842)
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 383 #molecular-weight 43936 #checksum 2897

Query Match 7.4%; Score 28; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 6,876-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 ILVPHGWRISHRTHQNHGVNDESM 150
QY 120 ILVPHGWRISHRTHQNHGVNDESM 147

RESULT 9
ENTRY JQ2335
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana
ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear cress
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 12-Mar-1999

ACCESSIONS JQ2335
REFERENCE T02487

potential protein-coding regions.

#cross-references M01D:97061201
#accession S75843
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-359 #label KAN
#cross-references EMBL:D90913; GB:AB001339; NID:g1653348; PID:d1019035;
PID:g1653388
#note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996

GENETICS
#start_codon GTC
#superfamily omega-3 fatty acid desaturase
#oxidoreductase
#length 359 #molecular-weight 41919 #checksum 9162

Query Match 4.2%; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 2,51e-21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPHGWRISHRTH 129
|||||
QY 120 ILVPHGWRISHRTH 135

RESULT 13 H71349 #type complete
ENTRY probable ribosomal protein L1 (rplA) - syphilis spirochete
TITLE #formal_name Treponema pallidum subsp. pallidum #common_name
ORGANISM syphilis spirochete
DATE 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
17-Mar-1999

ACCESSIONS H71349
REFERENCE A71250
#authors Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.;
Sutton, G.G.; Dodson, R.; Gwin, M.; Hickey, E.K.; Clayton,
R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod,
M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson,
D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonald,
L.; Artlach, P.; Bowman, C.; Cotton, M.D.; Fujii, C.;
Gairland, S.; Hatch, B.; Horst, K.; Roberts, K.; Matthey,
L.; Weidman, J.; Smith, H.O.; Venter, J.C.
#journal Complete genome sequence of Treponema pallidum, the syphilis
spirochete.
Science (1998) 281:375-388
#title
#cross-references M01D:98332770
#accession H71349
#status preliminary; nucleic acid sequence not shown;
translation not shown

GENETICS
#molecule_type DNA
#residues 1-226 #label COL
#cross-references GB:AE001205; GB:AE000520; NID:g3322501; PID:g3322508
#experimental_source strain Nichols

CLASSIFICATION TP0238
SUMMARY #superfamily Escherichia coli ribosomal protein L1
#length 226 #molecular-weight 24977 #checksum 6550

Query Match 2.1%; Score 8; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.91e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 83 ALAAGAY 90
|||||
QY 62 ALAAGAY 69

RESULT 14 S65770 #type complete
ENTRY maltotigosyltrehalose trehalohydrolase - Arthrobacter sp.
TITLE (strain Q36)
ORGANISM #formal_name Arthrobacter sp.
#variety strain Q36

DATE 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
18-Sep-1998

ACCESSIONS S65770
REFERENCE S65769
#authors Maruta, K.; Hattori, K.; Nakada, T.; Kubota, M.; Sugimoto,
T.; Kurimoto, M.
#journal Blochim. Biophys. Acta (1996) 1289:10-13
#title Cloning and sequencing of trehalose biosynthesis genes from
Arthrobacter sp. Q36.
#cross-references M01D:96195835
#accession S65770

GENETICS
#status preliminary
#molecule_type DNA
#residues 1-598 #label MAR
#cross-references EMBL:D63343; NID:g1255444; PID:d1010313; PID:g1255446
#superfamily trehalose trehalohydrolase
SUMMARY #length 598 #molecular-weight 65831 #checksum 4532

Query Match 2.1%; Score 8; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.91e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 EAAKPYLG 15
|||||
QY 317 EAAKPYLG 324

RESULT 15 S63399 #type complete
ENTRY probable membrane protein YNR067c - yeast (Saccharomyces
cerevisiae)
TITLE #formal_name Saccharomyces cerevisiae
ORGANISM 27-Apr-1996 #sequence_revision 03-May-1996 #text_change
14-Nov-1997

ACCESSIONS S63399
REFERENCE S62944
#authors Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.;
Hilbert, H.; Moestl, D.
#submission submitted to the Protein Sequence Database, April 1996
#accession S63399
#molecule_type DNA
#residues 1-1117 #label DUE
#cross-references EMBL:D71682; NID:g1302597; PID:e239600; PID:g1302598;
MIPS:YNR067c

GENETICS
#experimental_source strain S288c

KEYWORDS #map_position 14R
FEATURES
FEATURE 6-22 #domain transmembrane #status predicted #label TMM
SUMMARY #length 1117 #molecular-weight 121063 #checksum 7513

Query Match 2.1%; Score 8; DB 2; Length 1117;
Best Local Similarity 100.0%; Pred. No. 4.91e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 339 TVDSSSP 346
|||||
QY 2 TVDSSSP 9

Search completed: Sat Aug 21 12:24:17 1999
Job time : 60 secs.

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MSearch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:22:40 1999; Maspar time 11.12 Seconds

Tabular output not generated.

Title: >US-09-219-935-7
 Description: (1-378) from US09219935.pep
 Perfect Score: 378
 Sequence: 1 LTVDSSSSPRIEETKQRF.....DVIYVYADPNLXGELKYAE 378

Scoring table: TABLE uniprottable
 Gap 60

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 3.703; Variance 0.432; scale 8.566

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	378	100.0	404	1	PD3C_BRANA OMEGA-3 FATTY ACID DES	0.00e+00
2	103	27.2	446	1	PD3C_ARATH OMEGA-3 FATTY ACID DES	0.00e+00
3	42	11.4	435	1	PD3D_ARATH TEMPERATURE-SENSITIVE	1.99e-110
4	42	11.1	460	1	PD3C_RICCO OMEGA-3 FATTY ACID DES	5.10e-107
5	36	9.5	447	1	PD3C_SESIN OMEGA-3 FATTY ACID DES	9.53e-87
6	36	9.5	453	1	PD3C_SOYBN OMEGA-3 FATTY ACID DES	9.53e-87
7	28	7.4	377	1	PD31_BRANA OMEGA-3 FATTY ACID DES	2.52e-60
8	28	7.4	383	1	PD32_BRANA OMEGA-3 FATTY ACID DES	2.52e-60
9	28	7.4	386	1	PD3E_ARATH OMEGA-3 FATTY ACID DES	2.52e-60
10	27	7.1	380	1	PD3E_SOYBN OMEGA-3 FATTY ACID DES	4.36e-57
11	25	6.6	380	1	PD3E_PHAU OMEGA-3 FATTY ACID DES	1.14e-50
12	24	6.3	379	1	PD3E_TOBAC OMEGA-3 FATTY ACID DES	1.73e-47
13	8	2.1	326	1	RIL1_TREPA 50S RIBOSOMAL PROTEIN	1.92e-02
14	8	2.1	1117	1	YH96_YEAST HYPOTHETICAL 121.1 KD	1.92e-02
15	7	1.9	85	1	R127_STRGR 50S RIBOSOMAL PROTEIN	1.86e+00
16	7	1.9	100	1	CH10_THERH 10 KD CHAPERONIN (PROT	1.86e+00
17	7	1.9	112	1	AGN5_APLCA ABDOMINAL GANGLION NEU	1.86e+00
18	7	1.9	143	1	SYU_TORCA SYNTECTIN	1.86e+00
19	7	1.9	213	1	LEAL_HORVU ABA-INDUCIBLE PROTEIN	1.86e+00
20	7	1.9	232	1	Y08E_MYCTU HYPOTHETICAL 23.9 KD P	1.86e+00
21	7	1.9	236	1	LYSE_CORNL LYSINE EXPORTER PROTEI	1.86e+00
22	7	1.9	280	1	DUS7_RAT DUAL SPECIFICITY PROTE	1.86e+00
23	7	1.9	322	1	DUS7_HUMAN DUAL SPECIFICITY PROTE	1.86e+00

RESULT	1	STANDARD	PRT	404 AA.
ID	PD3C_BRANA			
AC	P48618;			
DT	01-FEB-1996 (REL. 33, CREATED)			
DI	01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)			
DE	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)			
DE	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-)			
GN	FAD7.			
OS	BRASSICA NAPUS (RAPE).			
OC	EUKARYOTA: VIRIDIPHYTES: EMBRYOPHYTES: TRACHEOPHYTES:			
OC	EUPHYLOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS; ROSIDAE;			
OC	CAPRARIACE; BRASSICACEAE; BRASSICA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SEED;			
RX	MEDLINE: 94302147.			
RA	YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,			
RA	KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWELGER B., STECCA K.L.,			
RA	ALLEN S.W., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,			
RA	FELDMANN K.A., PIERCE J., BROWSE J.;			
RT	Cloning of higher plant omega-3 fatty acid desaturases.;			
RT	PLANT PHYSIOL. 103:467-476(1993).			
CC	-1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES			
CC	THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY			
CC	ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT			
CC	TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS			
CC	ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.			
CC	-1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.			
CC	-1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).			
CC	-1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE			
CC	AND/OR BE INVOLVED IN METAL ION BINDING.			
CC	-1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.			
CC	*****			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	*****			
DR	EMBL, L22963; G408490; ALT_INIT.			
DR	PIR; P00812; P00812.			
DR	PRM; P00487; PA_desaturase; 1.			
KM	OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;			
KM	TRANSIT PEPTIDE.			

```
FT  NON_TER 1 1 CHLOROPLAST (POTENTIAL).
FT  TRANSIT <1 2 OMEGA-3 FATTY ACID DESATURASE,
FT  CHAIN ? 404 CHLOROPLAST.
FT  DOMAIN 121 125 HISTIDINE BOX 1.
FT  DOMAIN 157 161 HISTIDINE BOX 2.
FT  DOMAIN 324 328 HISTIDINE BOX 3.
SQ  SEQUENCE 404 AA; 46617 MW; 797F19FB CRC32;

Query Match 100.0%; Score 378; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 LTVSSSSPPIEEPKEKTRDPGAPPPNADIRAIKHCWKNPKMSGYVRELAIY 86
    |||||||
QY 1 LTVSSSSPPIEEPKEKTRDPGAPPPNADIRAIKHCWKNPKMSGYVRELAIY 60
    |||||||

Db 87 FALAAGAYLNNWLVWPLWYIAOGTMMFALVGLHDCGHSFSDNPRNSVGHLLHSSI 146
    |||||||
QY 61 FALAAGAYLNNWLVWPLWYIAOGTMMFALVGLHDCGHSFSDNPRNSVGHLLHSSI 120
    |||||||

Db 147 LVPYHGWRIISHRTIHQNHGVENDESMHPSSEKIKSLDKPTREFRFTPLVMLAPPYL 206
    |||||||
QY 121 LVPYHGWRIISHRTIHQNHGVENDESMHPSSEKIKSLDKPTREFRFTPLVMLAPPYL 180
    |||||||

Db 207 WARSFGKGSYHHPDSGLFLFKERNQVLTSTACTMAVLLVCLNFVGMQLKLYIY 266
    |||||||
QY 181 WARSFGKGSYHHPDSGLFLFKERNQVLTSTACTMAVLLVCLNFVGMQLKLYIY 240
    |||||||

Db 267 YWVNWMLDEFTYLLHHGHEDKLPYRGKEMSYLRGSLTTLDRDYGILNNHHIGTHVI 326
    |||||||
QY 241 YWVNWMLDEFTYLLHHGHEDKLPYRGKEMSYLRGSLTTLDRDYGILNNHHIGTHVI 300
    |||||||

Db 327 HHLFPOIPHYHLVEATEAKPYLGYREPKSGPLPHLLGLIAKSIEDHFVSDGDV 386
    |||||||
QY 301 HHLFPOIPHYHLVEATEAKPYLGYREPKSGPLPHLLGLIAKSIEDHFVSDGDV 360
    |||||||

Db 387 VYEADPNLYGEIKVTA 404
    |||||||
QY 361 VYEADPNLYGEIKVTA 378
    |||||||

RESULT 2
ID FD3D_ARATH STANDARD; PRT; 446 AA.
AC P46310;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7 OR FAD8.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC CAPRALES: BRASSICACEAE; ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=HYPOCOTYL;
RA MEDLINE: 94032147.
RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHMEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.;
RT Cloning of higher plant omega-3 fatty acid desaturases.
RL PLANT PHYSIOL. 103:467-476(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=AREAL PARTS;
RA MEDLINE: 94043239.
RA IBA K., GIBSON S., NISHIOUCHI T., FUSE T., NISHIMURA M., ARONDEL V.,
RA HUGLY S., SOMERVILLE C.R.;
RT "A gene encoding a chloroplast omega-3 fatty acid desaturase
complements alterations in fatty acid desaturation and chloroplast
```

```
RT copy number of the fad7 mutant of Arabidopsis thaliana.";
RL J. Biol. Chem. 268:24099-24105(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=HYPOCOTYL;
RA WATABIKI M., YAMAMOTO K.;
RL SUBMITTED (NOV-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERRODOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABE).
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; L22961; G408481; -
DR EMBL; D14007; G541653; -
DR EMBL; D26019; G468434; -
DR PFM; P00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW TRANSIT PEPTIDE.
FT TRANSIT 1
FT CHAIN ? 446 CHLOROPLAST (POTENTIAL).
FT DOMAIN 163 167 HISTIDINE BOX 1.
FT DOMAIN 199 203 HISTIDINE BOX 2.
FT DOMAIN 366 370 HISTIDINE BOX 3.
SQ SEQUENCE 446 AA; 51174 MW; 8DE08779 CRC32;

Query Match 27.2%; Score 103; DB 1; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPYINWMLDEFTYLLHHGHEDKLPYRGKEMSYLRGSLTTLDRDYGILNNHHIGTH 366
    |||||||
QY 239 IPYINWMLDEFTYLLHHGHEDKLPYRGKEMSYLRGSLTTLDRDYGILNNHHIGTH 298
    |||||||

Db 367 VIHHLFPOIPHYHLVEATEAKPYLGYREPKSGPLPHLL 409
    |||||||
QY 299 VIHHLFPOIPHYHLVEATEAKPYLGYREPKSGPLPHLL 341
    |||||||

RESULT 3
ID FD3D_ARATH STANDARD; PRT; 435 AA.
AC P48622;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
DE PRECURSOR (EC 1.14.99.-).
GN FAD8.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC CAPRALES; BRASSICACEAE; ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=AREAL PARTS;
RA MEDLINE: 95148742.
RA GIBSON S., ARONDEL V., IBA K., SOMERVILLE C.R.;
RT Cloning of a temperature-regulated gene encoding a chloroplast
```



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RT omega-3-desaturase from Arabidopsis thaliana.",
RL PLANT PHYSIOL. 106:1615-1621(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE=HYPOCOTYL;
RA WATAHAKI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
CC EMBL; L27158; G516045; -
CC DR EMBL; U08216; G497219; -
CC DR EMBL; D17578; G471093; -
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
CC TRANSIT PEPTIDE.
CC FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
CC FT CHAIN 1 435 TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID
CC FT FT DESATURASE, CHLOROPLAST.
CC FT DOMAIN 156 160 HISTIDINE BOX 1.
CC FT DOMAIN 192 196 HISTIDINE BOX 2.
CC FT DOMAIN 359 363 HISTIDINE BOX 3.
CC SQ SEQUENCE 435 AA; 50136 MW; 70613FE0 CRC32;

Query Match 11.4%; Score 43; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,99e-110;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 INNHHDIGTGVYHHLFPQIPHYHLEATEAKPYLGKYYRSP 391
Oy 288 INNHHDIGTGVYHHLFPQIPHYHLEATEAKPYLGKYYRSP 330

RESULT 4
ID FD3C_RICCO STANDARD; PRT; 460 AA.
AC P48619;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
DE PAD7A-1.
GN RICINUS COMMUNIS (CASTOR BEAN).
OS EUKARYOTA; VIRIDIPHYTA; STREPTOPHYTA; EMNRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC EUPHORBIALES; EUPHORBIACEAE; RICINUS.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-CV. BAKER 296; TISSUE=SEED;
RX MEDLINE: 94302177.
RA VAN DE LOO F.J., SOMERVILLE C.R.;
RT "Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.";
CC CC PLANT PHYSIOL. 105:443-444(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; L25897; GA14732; -.
CC DR PFAM; PF00487; FA_desaturase; 1.
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
CC TRANSIT PEPTIDE.
CC FT TRANSIT 1.
CC FT CHAIN ? 460 CHLOROPLAST (POTENTIAL),
CC FT ? OMEGA-3 FATTY ACID DESATURASE,
CC FT CHLOROPLAST.
CC FT DOMAIN 177 181 HISTIDINE BOX 1.
CC FT DOMAIN 213 217 HISTIDINE BOX 2.
CC FT DOMAIN 380 384 HISTIDINE BOX 3.
CC SQ SEQUENCE 460 AA; 52561 MW; DB3DB689 CRC32;
CC -----
Cc Query Match 11.1%; Score 42; DB 1; Length 460;
Cc Best Local Similarity 100.0%; Pred. NO. 5,10e-107;
Cc Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cc -----
Cc Db 190 LNSVYGLHSHSILVYHGMRISRTHQHNGHVENDESWP 231
Cc 108 LNSVYGLHSHSILVYHGMRISRTHQHNGHVENDESWP 149
Cc -----
Cc RESULT 5 STANDARD: PRT: 447 AA.
Cc ID FD3C_SESIN P46620.
Cc AC 01-FEB-1996 (REL. 33, CREATED)
Cc DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
Cc DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
Cc DE OMEGA-3 FATTY ACID DESATURASE. CHLOROPLAST PRECURSOR (EC 1.14.99.-).
Cc FM 1997.
Cc GN SESAMUM INDICUM (ORIENTAL SESAME) (GINGELLY).
Cc OC EUPARROTIA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
Cc CC EUPHYLLIPHYTES; SPEMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
Cc CC ASPERIDAE; GENTIANANAE; LAMIALES; PEDALIACEAE; SESAMUM.
Cc CC [1]
Cc RN SEQUENCE FROM N.A.
Cc RP STRAIN-CV. 4294; TISSUE-COTYLEDON;
Cc RC SHOJI K.;
Cc RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
Cc CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
Cc THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
Cc ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
Cc TO USE PEREROXOXYN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
Cc ESERIFIED TO GALACTOLIPIDS, SULFOIPIDS AND PHOSPHATIDYLGLYCEROL.
Cc CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
Cc CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
Cc CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
Cc AND/ OR BE INVOLVED IN METAL ION BINDING.
Cc CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
Cc -----
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Cc or send an email to license@isb-sib.ch).
Cc -----
Cc EMBL; U25817; G870784; -.
Cc PFAM; PF00487; FA_desaturase; 1.

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KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW TRANSIT PEPTIDE. 1.
FT CHAIN ? 447 CHLOROPLAST (POTENTIAL).
FT CHAIN ? 447 OMEGA-3 FATTY ACID DESATURASE,
CHLOROPLAST.
FT DOMAIN 167 171 HISTIDINE BOX 1.
FT DOMAIN 203 207 HISTIDINE BOX 2.
FT DOMAIN 370 374 HISTIDINE BOX 3.
SQ SEQUENCE 447 AA; 5116 MW; 67B2C46B CRC32;
Query Match 9.5%; Score 36; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 9.53e-87;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 323 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 358
251 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 286
RESULT 6
ID FD3C_SOYBN STANDARD; PRT: 453 AA.
AC P48621;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7.
OS GLYCINE MAX (SOYBEAN).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RX MEDLINE: 94302147.
RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R., JR., SCHMEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMANN K.A., PIERCE J., BROWSE J.;
RT Cloning of higher plant omega-3 fatty acid desaturases.";
RT PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASES."
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L22965; G408792; -.
DR PRAM: PF00487; FA.desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT CHAIN 1 ? 453 CHLOROPLAST (POTENTIAL).
FT CHAIN 1 ? 453 OMEGA-3 FATTY ACID DESATURASE,
CHLOROPLAST.
FT DOMAIN 171 175 HISTIDINE BOX 1.
FT DOMAIN 207 211 HISTIDINE BOX 2.
FT ~DOMAIN 374 378 HISTIDINE BOX 3.
SQ SEQUENCE 453 AA; 51362 MW; E431AF1B CRC32;

Query Match 9.5%; Score 36; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 9.53e-87;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 327 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 362
251 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 286
RESULT 7
ID FD3L_BRANA STANDARD; PRT: 377 AA.
AC P46311;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
GN (VERSION 1).
GN FAD3.
OS BRASSICA NAPUS (RAPE).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPPALES; BRASSICACEAE; BRASSICA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RX MEDLINE: 94302147.
RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R., JR., SCHMEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMANN K.A., PIERCE J., BROWSE J.;
RT Cloning of higher plant omega-3 fatty acid desaturases.";
RT PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL: L22962; G408492; -.
DR PRAM: PF00487; FA.desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KM TRANSMEMBRANE.
FT TRANSMEM 54 73 POTENTIAL.
FT TRANSMEM 203 226 POTENTIAL.
FT TRANSMEM 233 251 POTENTIAL.
FT DOMAIN 92 96 HISTIDINE BOX 1.
FT DOMAIN 128 132 HISTIDINE BOX 2.
FT DOMAIN 295 299 HISTIDINE BOX 3.
SQ SEQUENCE 377 AA; 43258 MW; 247237E0 CRC32;
Query Match 7.4%; Score 28; DB 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.52e-60;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 117 ILVYHGMRISHRTHQNHGVNDESM 144
120 ILVYHGMRISHRTHQNHGVNDESM 147

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RESULT 8
ID FD32_BRANA STANDARD; PRT: 363 AA.
AC P48624;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASTIC RETICULUM (EC 1.14.99.-)
DE (VERSION 2).
GN FAD3.
OS BRASSICA NAPUS (RAPE).
OC EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES:
OC EUPHYLOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS: ROSIDAE:
CAPPALES; BRASSICACEAE; BRASSICA.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 93080059.
RA ARONDEL V., LEMIEUX B., HWANG I., GIBSON S., GOODMAN H.M.,
RA SOMERVILLE C.R.;
RT Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis.*;
RL SCIENCE 258:1353-1355(1992).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL: L01418; G167148; -.
CC DR PRAM; PF00487; FA,desaturase; 1.
CC KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC TRANSMEMBRANE.
CC FT TRANSMEM 53 73 POTENTIAL.
CC FT TRANSMEM 210 230 POTENTIAL.
CC FT TRANSMEM 234 254 POTENTIAL.
CC FT DOMAIN 98 102 HISTIDINE BOX 1.
CC FT DOMAIN 134 138 HISTIDINE BOX 2.
CC FT DOMAIN 301 305 HISTIDINE BOX 3.
CC SQ SEQUENCE 363 AA; 43936 MW; F39A878B CRC32;

Query Match 7.4%; Score 28; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 2,52e-60;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 ILVPHGMRIHRTNHNHGHVDESW 150
OY 120 ILVPHGMRIHRTNHNHGHVDESW 147

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OC CAPPALES; BRASSICACEAE; ARABIDOPSIS.
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA; TISSUE-SEEDLING;
RX MEDLINE: 94302147.
RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.;
RT Cloning of higher plant omega-3 fatty acid desaturases.*;
RL PLANT PHYSIOL. 103:467-476(1993).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA; TISSUE-HYPOCOTYL;
RA WATAHAKI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA;
RX MEDLINE: 94345020.
RA NISHITUCHI T., NISHIMURA M., ARONDEL V., IBA K.;
RT Genomic nucleotide sequence of a gene encoding a microsomal omega-3
RT fatty acid desaturase from Arabidopsis thaliana.*;
RL PLANT PHYSIOL. 105:767-768(1994).
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA;
RA ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
RA STRES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
RA SOMERVILLE C.R., YENTER J.C.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: MICROSOAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
CC DETECTABLE IN ROOT TISSUE.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC EMBL: L22931; G408483; -.
CC DR EMBL; D17579; G471091; -.
CC DR EMBL; D26508; G1197795; -.
CC DR EMBL; AC004680; G3420053; -.
CC PRAM; PF00487; FA,desaturase; 1.
CC KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC TRANSMEMBRANE.
CC FT TRANSMEM 63 83 POTENTIAL.
CC FT TRANSMEM 220 240 POTENTIAL.
CC FT TRANSMEM 242 262 POTENTIAL.
CC FT DOMAIN 101 105 HISTIDINE BOX 1.
CC FT DOMAIN 137 141 HISTIDINE BOX 2.
CC FT DOMAIN 304 308 HISTIDINE BOX 3.
CC SQ SEQUENCE 386 AA; 44076 MW; C22B4B8C CRC32;

Query Match 7.4%; Score 28; DB 1; Length 386;
Best Local Similarity 100.0%; Pred. No. 2,52e-60;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 ILVPHGMRIHRTNHNHGHVDESW 153

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OY 120 ILVPHGMRIHSRTHQNHGVNDESW 147

RESULT 10
ID FD3E_S0YBN STANDARD: PRT: 380 AA.
AC P48625:
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
GN FAD3.
OS GLYCINE MAX (SOYBEAN).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC FABALES: FABACEAE: PAPILIONOIDEAE: GLYCINE.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED:
RA MEDLINE: 94302147.
RA YADAV N.S., WIERBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROSE J.:
RT "Cloning of higher plant omega-3 fatty acid desaturases."
RL PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL: L22964; G408794; -.
DR PIR: J02338; J02338.
DR PFAM: PF00487; FA_desaturase; 1.
DR OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 100 104 HISTIDINE BOX 1.
FT DOMAIN 136 140 HISTIDINE BOX 2.
FT DOMAIN 303 307 HISTIDINE BOX 3.
FT SEQUENCE 380 AA; 44185 MW; E3C509B7 CRC32;

Query Match 7.1%; Score 27; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 4,36e-57;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 295 NIHHDIGTHVHHLFPOIPHYLVEAT 321
OY 290 NIHHDIGTHVHHLFPOIPHYLVEAT 316

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DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).
GN ARG1.
OS PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC FABALES: FABACEAE: PAPILIONOIDEAE: VIGNA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOCOTYL.
RA YAMAMOTO K.T., MORI H., IMASEKI H.:
RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
RT elongating hypocotyls of mung bean (Vigna radiata).".
RL PLANT CELL PHYSIOL. 33:13-20(1992).
CC -1- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
DR EMBL: D14410; G287562; -.
DR PFAM: PF00487; FA_desaturase; 1.
DR OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 59 78 POTENTIAL.
FT TRANSMEM 208 231 POTENTIAL.
FT TRANSMEM 238 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
FT SEQUENCE 380 AA; 43996 MW; 8429BF68 CRC32;

Query Match 6.6%; Score 25; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.14e-50;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 294 HHHDIGTHVHHLFPOIPHYLVEAT 318
OY 292 HHHDIGTHVHHLFPOIPHYLVEAT 316

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RA HAMADA T., KODAMA H., NISHIMURA M., IBA K.:
 RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase."
 RL GENE 147:293-294(1994).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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 CC -----
 CC EMBL: D26509; G599592; -
 CC DR PFAM: PF00487; FA_desaturase; 1.
 CC KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 CC TRANSMEMBRANE.
 CC FT TRANSMEM 52 72 POTENTIAL.
 CC FT TRANSMEM 213 233 POTENTIAL.
 CC FT TRANSMEM 236 236 POTENTIAL.
 CC FT DOMAIN 97 101 HISTIDINE BOX 1.
 CC FT DOMAIN 133 137 HISTIDINE BOX 2.
 CC FT DOMAIN 300 304 HISTIDINE BOX 3.
 CC SQ SEQUENCE 379 AA; 44149 MW; C237E46D CRC32;
 CC -----
 CC Query Match 6.3%; Score 24; DB 1; Length 379;
 CC Best Local Similarity 100.0%; Pred. No. 1,73e-47;
 CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC Db 291 NNTHDICTVHHLFPOIPHYHL 314
 CC QY 289 NNTHDICTVHHLFPOIPHYHL 312
 CC -----
 CC RESULT 13
 CC ID RL1 TREPA STANDARD; PRT; 226 AA.
 CC AC 083266;
 CC DT 15-DEC-1998 (REL. 37, CREATED)
 CC DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
 CC DE 50S RIBOSOMAL PROTEIN L1.
 CC GN RPLA OR TP0238.
 CC OS TREPONEMA PALLIDUM.
 CC OC BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; TREPONEMA.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-NICHOLS;
 CC RX MEDLINE: 98332770.
 CC RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 CC DODGSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
 CC SODERGREN E., HARDAM J.M., MCLEOD M.P., SALBERG S., PETERSON J.,
 CC KHALAK H., RICHARDSON D., HOWELL J.K., CHIDABARAM M., UTTERBACK T.,
 CC MC DONALD L., ARTICH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
 CC HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
 CC VENTER J.C.;
 CC RT "Complete genome sequence of Treponema pallidum, the syphilis
 CC spirochete."
 CC RL SCIENCE 281:375-388(1998).
 CC CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
 CC LOCATED IN THE NEIGHBORHOOD OF THE SITE WHERE ELONGATION FACTOR TU
 CC IS BOUND TO THE RIBOSOME (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LIP FAMILY OF RIBOSOMAL PROTEINS.
 CC -----

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 CC -----
 CC DR EMBL: AE001205; G322508; -
 CC DR TIGR: TP0238;
 CC DR PROSITE: PS01199; RIBOSOMAL_L1; 1.
 CC KM RIBOSOMAL PROTEIN; RNA-BINDING.
 CC SQ SEQUENCE 226 AA; 24977 MW; 423DF8A1 CRC32;
 CC -----
 CC Query Match 2.1%; Score 8; DB 1; Length 226;
 CC Best Local Similarity 100.0%; Pred. No. 1,92e-02;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC Db 83 ALAAGAY 90
 CC QY 62 ALAAGAY 69
 CC -----
 CC RESULT 14
 CC ID YN96_YEAST STANDARD; PRT; 1117 AA.
 CC AC P53753;
 CC DT 01-OCT-1996 (REL. 34, CREATED)
 CC DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 CC DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 CC DE HYPOTHEICAL 121.1 KD PROTEIN IN BIO3-HXT17 INTERGENIC REGION
 CC DE PRECURSOR.
 CC GN YN9607C OR N3547.
 CC OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 CC OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYTES; SACCCHAROMYCETALES;
 CC OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RA DUESTERHOEFT A., FLOETH M., FRITZ C., HEUSS-NEITZEL D.,
 CC HILBERT H., MOESTL D.;
 CC RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC CC -1- SIMILARITY: TO YEAST YNR144C AND S.POMBE SPAC23D3.10C.
 CC -----
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 CC -----
 CC DR EMBL: Z71682; E238600; -
 CC KM HYPOTHEICAL PROTEIN; GLYCOPROTEIN; SIGNAL.
 CC FT SIGNAL 1 16
 CC FT CHAIN 17 1117
 CC FT DOMAIN 342 345
 CC FT DOMAIN 345 370
 CC FT DOMAIN 376 383
 CC FT DOMAIN 376 383
 CC FT CARBOHYD 138 138
 CC FT CARBOHYD 186 186
 CC FT CARBOHYD 223 223
 CC FT CARBOHYD 223 223
 CC FT CARBOHYD 259 259
 CC FT CARBOHYD 280 280
 CC FT CARBOHYD 303 303
 CC FT CARBOHYD 307 307
 CC FT CARBOHYD 333 333
 CC FT CARBOHYD 333 333
 CC FT CARBOHYD 533 533
 CC FT CARBOHYD 866 866
 CC SQ SEQUENCE 1117 AA; 121063 MW; 9AB486C6 CRC32;
 CC -----
 CC Query Match 2.1%; Score 8; DB 1; Length 1117;
 CC Best Local Similarity 100.0%; Pred. No. 1,92e-02;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----

Db 339 TVDSSSP 346
 |||||
 QY 2 TVDSSSP 9

RESULT 15
 ID RU27_STRGR STANDARD: PRT: 85 AA.

AC P95757;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE 50S RIBOSOMAL PROTEIN L27.

GN RPA.
 OS STREPTOMYCES GRISEUS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-IFO 13189.
 RX MEDLINE; 97136618.

RA OKAMOTO S., ITOH M., OCHI K.;

RT "Molecular cloning and characterization of the obp gene of
 RT Streptomyces griseus in relation to the onset of morphological
 RT differentiation";

RL J. BACTERIOL. 179:170-179(1997).

CC -1- SIMILARITY: BELONGS TO THE L27P FAMILY OF RIBOSOMAL PROTEINS.

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CC -----

CC EMBL: D87916; G1783293; -

DR PROSITE; PS00831; RIBOSOMAL_L27; 1.

DR Pfam; PF01016; Ribosomal_L27; 1.

KW RIBOSOMAL PROTEIN.

SO SEQUENCE 85 AA; 8860 MW; 804E9523 CRC32;

Query Match 1.9%; Score 7; DB 1; Length 85;
 Best Local Similarity 100.0%; Pred.No.1.86e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 FALAGA 66
 |||||
 QY 61 FALAGA 67

Search completed: Sat Aug 21 12:22:59 1999
 Job time : 19 secs.


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RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-HONEY BANTAM AND HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
DR EMBL: D84409; D1023307; -.
DR EMBL: D63953; D1023305; -.
DR PFM: PF00487; FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 398 AA; 44789 MW; 70565EEC CRC32;

Query Match 11.4%; Score 43; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 1,52e-104;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 EMSYLRGSLTLDRDYGILNNIHHDIGTHVHILFPQIPHYHL 333
YQ 270 EMSYLRGSLTLDRDYGILNNIHHDIGTHVHILFPQIPHYHL 312

RESULT 3
ID 082068; PRELIMINARY; PRT; 431 AA.
AC 082068;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE W-3 DESATURASE.
OS SOLANUM TUBEROSUM (POTATO);
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; SOLANUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RA LEON J.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RA MARTIN M.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ007739; E1318202; -.
SQ SEQUENCE 431 AA; 49253 MW; BAF9F9CD CRC32;

Query Match 10.6%; Score 40; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.72e-95;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 345 INNTHHDIGTHVHILFPQIPHYHLEATEAKPVLGKYY 384
YQ 288 INNTHHDIGTHVHILFPQIPHYHLEATEAKPVLGKYY 327

RESULT 4
ID P93350; PRELIMINARY; PRT; 441 AA.
AC P93350;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
GN NFEAD7.
OS NICOTIANA TABACUM (COMMON TOBACCO);
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; NICOTIANA.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 96416425.
RA HAMADA T., NISHITUCHI T., KODAMA H., NISHIMURA M., IBA K.;
RT "cDNA cloning of a wounding-inducible gene encoding a plastid omega-3
fatty acid desaturase from tobacco";
RL PLANT CELL PHYSIOL. 37:606-611(1996).
DR EMBL: D79979; D1012141; -.
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DR PFM: PF00487; FA_desaturase; 1.
DR MENDEL; 9312; NICtA;1208;2.
SQ SEQUENCE 441 AA; 50310 MW; 255F96A6 CRC32;

Query Match 10.6%; Score 40; DB 10; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.72e-95;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 355 INNTHHDIGTHVHILFPQIPHYHLEATEAKPVLGKYY 394
YQ 288 INNTHHDIGTHVHILFPQIPHYHLEATEAKPVLGKYY 327

RESULT 5
ID 004807; PRELIMINARY; PRT; 438 AA.
AC 004807;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PERILLA FRUTESCENS.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANACEAE; LAMIALES; LAMIACEAE; PERILLA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ORDONG;
RA LEE S.K., KIM K.H., KIM Y.M., HWANG Y.S.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U58477; G1754795; -.
DR PFM: PF00487; FA_desaturase; 1.
DR MENDEL; 16268; PERlt;1208;mm16268.
SQ SEQUENCE 438 AA; 50160 MW; EE726819 CRC32;

Query Match 9.8%; Score 37; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 2.54e-85;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 GHLHSSILVPHGWRISRTTHONHGVNDESWHP 217
YQ 113 GHLHSSILVPHGWRISRTTHONHGVNDESWHP 149

RESULT 6
ID 023824; PRELIMINARY; PRT; 443 AA.
AC 023824;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE.
GN FAD7.
OS ZEAMAYS (MAIZE).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
RN [2]
RP SEQUENCE OF 182-443 FROM N.A.
RC STRAIN-HONEY BANTUM;
RX MEDLINE; 98145435.
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RT "Two maize genes encoding omega-3 fatty acid desaturase and their
differential expression to temperature.";
RL PLANT MOL. BIOL. 36:297-306(1998).
DR EMBL: D63954; D1023306; -.
DR EMBL: D63952; D1023304; -.
DR PFM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 443 AA; 49437 MW; E8BC6757 CRC32;
```


RA IBA K.;
RL PHYSIOL. PLANTARUM 96:275-283(1996).
DR EMBL: D43688; D1008371; -.
DR PFAM: PF00487; FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 380 AA; 42633 MW; 2123FF56 CRC32;

Query Match 6.3%; Score 24; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 5,77e-45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 130 GWRISHRTHONHGHVDESWHP 153
126 GWRISHRTHONHGHVDESWHP 149
|||||

RESULT 12 PRELIMINARY; PRT; 359 AA.
ID 055240;
AC 055240;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE DELTA 15 DESATURASE.
GN DESB.
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95035996.
RA SAKAMOTO T., LOS D.A., HIGASHI S., WADA H., NISHIDA I., OHMORI M.,
RA MURATA N.,
RT "Cloning of omega 3 desaturase from cyanobacteria and its use in
RT altering the degree of membrane-lipid unsaturation.";
RL PLANT MOL. BIOL. 26:249-263(1994).
[2]
RP SEQUENCE FROM N.A.
RA TABATA S.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAKOTO S., KIMURA T.,
RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
RA TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA RES. 3:109-136(1996).
DR EMBL: D13780; G600598; -.
DR EMBL: D90913; G1653388; -.
DR PFAM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 359 AA; 41919 MW; B5375D98 CRC32;

Query Match 4.2%; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 8,34e-22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPHGWRISHRTH 129
120 ILVPHGWRISHRTH 135
|||||

RESULT 13 PRELIMINARY; PRT; 350 AA.
ID 007872;
AC 007872;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE -OMEGA-3-DESATURASE.
GN DESB.
OS SYNECHOCOCUS PCC7002.

OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCOCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97260123.
RA SAKAMOTO T., BRYANT D.A.;
RT "Temperature-regulated mRNA accumulation and stabilization for fatty
RT acid desaturase genes in the cyanobacterium Synechococcus sp. strain
RT PCC 7002.";
RL MOL. MICROBIOL. 23:1281-1292(1997).
DR EMBL: U36389; G2197199; -.
DR PFAM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 350 AA; 40562 MW; 969CAD61 CRC32;

Query Match 2.9%; Score 11; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 8,89e-09;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 AOGTFFWALFY 84
82 AOGTFFWALFY 92
|||||

RESULT 14 PRELIMINARY; PRT; 193 AA.
ID 074645;
AC 074645;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
OS GIBBERELLA ZEAE.
OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
OC HYPOCREALES; HYPOCREACEAE; GIBBERELLA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-F15;
RX MEDLINE: 98433864.
RA KIMURA M., MATSUMOTO G., SHINGU Y., YONEYAMA K., YAMAGUCHI I.;
RT "The mystery of the trichothecene 3-O-acetyltransferase gene.
RT Analysis of the region around Trl01 and characterization of its
RT homologue from Fusarium sporotrichoides.";
RL FEBS LETT. 435:163-168(1998).
DR EMBL: AB014492; D1034743; -.
FT NON_TER 1
FT NON_TER 193
SQ SEQUENCE 193 AA; 21845 MW; BF2053ED CRC32;

Query Match 2.1%; Score 8; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 4,64e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 186 HVHHLFP 193
298 HVHHLFP 305
|||||

RESULT 15 PRELIMINARY; PRT; 598 AA.
ID 044316;
AC 044316;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE MALTOLOGOSYL TREHALOSE TREHALOHYDROLASE.
GN TREZ.
OS ARTHROBACTER SP.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIAE;
OC ACTINOMYCETEALES; MICROCOCCINEAE; MICROCOCCACEAE; ARTHROBACTER.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Q36;
RX MEDLINE: 96195835.
RA MARUTA K., HATORI K., NAKADA T., KUBOTA M., SUGIMOTO T., KURIMOTO M.;
RT "Cloning and sequencing of trehalose biosynthesis genes from
RT Arthrobacter sp. Q36.";

```

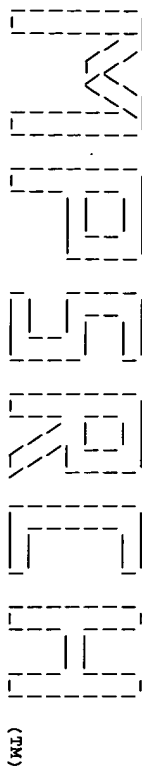
?
RL BIOCIM, BIOCIM, ACTA 1289:10-13(1996).
DR EMBL; D63343; D1010313;
DR PFAM; PF00128; alpha-amylase; 1.
KW HYDROLASE.
SQ SEQUENCE 598 AA; 65832 MW; 22719107 CRC32;

Query Match      2.18; Score 8; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 4,64e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      8 EAAKPYLG 15
      |||||
QY      317 EAAKPYLG 324
  
```

Search completed: Sat Aug 21 12:26:12 1999
 Job time : 98 secs.

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Msearch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:18:17 1999; Maspar time 15.09 Seconds

Tabular output not generated. 532.719 Million cell updates/sec

Title: >US-09-219-935-7

Description: (1-378) from US0921935.pep

Perfect Score: 378

Sequence: 1 LTVDSSTSPTEEPKTRF.....DVVYVADPNLGEIKYAE 378

Scoring table: TABLE uniprottable

Gap 60

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseg35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 2.891; Variance 0.684; scale 4.229

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	378	100.0	378	7	R37591	Sequence of microsoma
2	378	100.0	404	7	R37594	Sequence of plastid d
3	103	27.2	446	11	R60499	Linoleic-acid-desatur
4	103	27.2	446	7	R37593	Sequence of a plastid
5	43	11.4	435	11	R60500	Linoleic-acid-desatur
6	36	9.5	447	24	W13381	Sesame omega-3 alpha
7	36	9.5	453	7	R37596	Sequence of soybean p
8	30	7.9	156	7	R37598	Sequence of a plastid
9	28	7.4	383	11	R60498	Linoleic-acid-desatur
10	28	7.4	386	7	R37592	Sequence of delta-15
11	27	7.1	380	7	R37595	Sequence of microsoma
12	27	7.1	125	7	R37597	Sequence of an intern
13	9	2.4	387	10	R37600	Sequence of corn mler
14	8	2.1	20	14	R80294	Trehalose releasing e
15	8	2.1	597	14	R80290	Trehalose releasing e
16	8	2.1	598	14	R77471	Trehalose releasing e

Result	ID	Score	Query Match	Length	ID	Description	Pred. No.
17	7	1.9	18	17	R88585	Spider venom calcium	1.76e+01
18	7	1.9	18	2	R07633	N-terminal of Fractio	1.76e+01
19	7	1.9	18	8	R38424	A.aperta venom Fractio	1.76e+01
20	7	1.9	236	26	W37715	C. glutamicum Lys E p	1.76e+01
21	7	1.9	289	19	W01128	Coat protein (short v	1.76e+01
22	7	1.9	367	19	R98899	Coat protein (long ve	1.76e+01
23	7	1.9	367	34	W61492	Human fetuin glycopro	1.76e+01
24	7	1.9	663	4	R24101	Marek's disease virus	1.76e+01
25	6	1.6	202	39	W67822	Human secreted protei	2.35e+02
26	6	1.6	203	39	W67898	Human secreted protei	2.35e+02
27	6	1.6	239	36	W80690	S. pneumoniae protein	2.35e+02
28	6	1.6	248	5	R25573	Mature alpha-Tri-chosa	2.35e+02
29	6	1.6	267	23	W21703	H. pylori secreted or	2.35e+02
30	6	1.6	373	22	W20833	Human growth-related	2.35e+02
31	6	1.6	424	38	W86150	B. subtilis Yade rela	2.35e+02
32	6	1.6	438	39	W95500	Human protein-couple	2.35e+02
33	6	1.6	493	39	W84068	Human mitochondriin Fzo h	2.35e+02
34	6	1.6	519	39	W89782	Staphylococcus aureus	2.35e+02
35	6	1.6	539	37	W76281	Coprinus cinereus lac	2.35e+02
36	6	1.6	549	38	W70898	Acetyl-coenzyme A tra	2.35e+02
37	6	1.6	707	38	W83395	Rabbit protein-couple	2.35e+02
38	6	1.6	708	38	W83394	Human protein-couple	2.35e+02
39	6	1.6	844	19	R86952	E. coli PBP 1B transg	2.35e+02
40	6	1.6	1012	39	W95395	IBDV VP2-VP3-VP4 poly	2.35e+02
41	6	1.6	1978	35	W69361	Tetradotoxin-sensitiv	2.35e+02
42	6	1.6	1988	35	W69362	Tetradotoxin-sensitiv	2.35e+02
43	6	1.6	2100	39	W89579	Calcium permeable vol	2.35e+02
44	6	1.6	2104	39	W89578	Calcium permeable vol	2.35e+02
45	6	1.6	2105	39	W89577	Calcium permeable vol	2.35e+02

ALIGNMENTS

RESULT 1
ID R37591 standard; Protein; 378 AA.
AC R37591;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone PBNSF3-f2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPC) DU POINT DE NEMOURS & CO E. I.
PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR NPI: 93-197063/24.
DR N-PSDB: 043205.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 136-138; 167pp; English.
CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from pCF3 and pCM2 were used to isolate PBNSF3-2. Plasmid PBNSF3-2
CC was deposited as ATCC No. 68854. PBNSF3-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 378 AA:
Query Match 100.0%; Score 378; Length 378;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ltvdsassppieepkqrfdbgappfnadiraalpkhwnkpwmsyvvrelaiiv 60
   1 LTVSSSSPPIEEBPKTORFDPGAPPPNLADIRAIPIKHWKVMKMSKSYVRELAIIV 60
Qy 61 falaagaaylwnwlvwplwylwaggtmfwalfvlgdhcghsfnsndprlnsvvghllhss1 120
   61 FALAAGAAYLWNWLVWPLWYLVWAGGTMFVALFVLGHCCHGSFNSNDPRLNSVVGHLHSSI 120
Db 121 lvpvhwgrishrthqnhghvendeswhpmseklyksldkptcrrffrtflplwmlayfpyl 180
   121 LVPVHWGRISHRTHQHNGHVENDESWHPMSEKITYKSLDKPTRFRFTPLPLWMLAYFPYL 180
Qy 181 warspgkgsghyhpdsdlflpkerndvltstacwtamaavlvclnfvmgmqmklyvip 240
   181 WARSFGKGSYHHPDSDLFLPKERNVDLTSTACWTAMAAVLVCLNFVGMQMMLKLYVIP 240
Db 241 ywlnvwmldfvtlylhhghedklpwyrgekwsylrgslttldrdyglinnihhdigthvi 300
   241 YWLNVMWLDFTVLYLHHGHEDKLPWYRGKESYLRGSLTTLDRODGLINNIIHHDIGTHVI 300
Qy 301 hnlfpqiphylveateaakpvlqkyrepdksgpplhllgilaaksikedhfvdsedgv 360
   301 HNLFPQIPHYLVATEAAKPVLGKYREPKSGPLRLHLGLIAKSIKEDHFVDSGDV 360
Db 361 vyaeadpnllygelkvtae 378
   361 VYEADPNLYGEIKVTAE 378
Qy 361 VYEADPNLYGEIKVTAE 378

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```

RESULT 2
ID R37594 standard; Protein; 404 AA.
AC R37594;
DE 01-OCT-1993 (first entry)
DT Sequence of plastid delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone PBNSF-2.
PN W09311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO.) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
PI WPI: 93-197063/24.
DR N-PSDB: Q43206.
PT Isolated nucleic acid fragment, for plant lipid composn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 140-141; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from PCF3 and PCM2 were used to isolate PBNSF3-2. The cDNA inserts
CC was deposited at ATCC No. 68854. PBNSF-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 404 AA;

```

```

Query Match 100.0%; Score 378; DB 7; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.0e+00;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 27 ltvdsassppieepkqrfdbgappfnadiraalpkhwnkpwmsyvvrelaiiv 86
   1 LTVSSSSPPIEEBPKTORFDPGAPPPNLADIRAIPIKHWKVMKMSKSYVRELAIIV 60
Qy 1 LTVSSSSPPIEEBPKTORFDPGAPPPNLADIRAIPIKHWKVMKMSKSYVRELAIIV 60

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Db 87 falaagaaylwnwlvwplwylwaggtmfwalfvlgdhcghsfnsndprlnsvvghllhss1 146
   61 FALAAGAAYLWNWLVWPLWYLVWAGGTMFVALFVLGHCCHGSFNSNDPRLNSVVGHLHSSI 120
Qy 147 lvpvhwgrishrthqnhghvendeswhpmseklyksldkptcrrffrtflplwmlayfpyl 206
   121 LVPVHWGRISHRTHQHNGHVENDESWHPMSEKITYKSLDKPTRFRFTPLPLWMLAYFPYL 180
Db 207 warspgkgsghyhpdsdlflpkerndvltstacwtamaavlvclnfvmgmqmklyvip 266
   181 WARSFGKGSYHHPDSDLFLPKERNVDLTSTACWTAMAAVLVCLNFVGMQMMLKLYVIP 240
Qy 241 ywlnvwmldfvtlylhhghedklpwyrgekwsylrgslttldrdyglinnihhdigthvi 300
   241 YWLNVMWLDFTVLYLHHGHEDKLPWYRGKESYLRGSLTTLDRODGLINNIIHHDIGTHVI 300
Db 327 hnlfpqiphylveateaakpvlqkyrepdksgpplhllgilaaksikedhfvdsedgv 386
   301 HNLFPQIPHYLVATEAAKPVLGKYREPKSGPLRLHLGLIAKSIKEDHFVDSGDV 360
Qy 387 vyaeadpnllygelkvtae 404
   361 VYEADPNLYGEIKVTAE 378

```

```

RESULT 3
ID R60499 standard; Protein; 446 AA.
AC R60499;
DE 28-MAR-1995 (first entry)
DT Lipoic-acid-desaturase fadd.
KW Lipoic-acid-desaturase; fadd; transgenic plant; crop improvement;
KW lipoic acid.
OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PE 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS.) MONSANTO CO.
PA (UNMS.) UNIV MICHIGAN STATE.
PI Aronides VJA, Gibson ST, Kishore GM, Ruff TG, Somerville CR;
PI WPI: 94-279758/34.
DR N-PSDB: Q71210.
PT Genetically transformed plants with altered lipoic acid
PT content - contg recombinant, double-stranded DNA encoding
PT lipoic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 75-77; 144pp; English.
CC The cDNA sequence and deduced amino acid sequence of lipoic-acid-
CC acid-desaturase fadd of Arabidopsis are provided.
SQ Sequence 446 AA;

```

```

Query Match 27.2%; Score 103; DB 11; Length 446;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 307 lpyvlnvwmldfvtlylhhghedklpwyrgekwsylrgslttldrdyglinnihhdigth 366
   239 lpyvlnvwmldfvtlylhhghedklpwyrgekwsylrgslttldrdyglinnihhdigth 298
Qy 239 lpyvlnvwmldfvtlylhhghedklpwyrgekwsylrgslttldrdyglinnihhdigth 298

```

```

RESULT 4
ID R37593 standard; Protein; 446 AA.
AC R37593;
DE 01-OCT-1993 (first entry)
DT Sequence of a plastid delta-15 fatty acid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone PACF2-2.
PN W09311245-A.

```

PD 10-JUN-1993.
 PF 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB; Q43204.
 PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure; Page 132-134; 167pp; English.
 CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. In contrast to the
 CC constitutive expression of the gene encoding (R37592), the mRNA
 CC corresponding to Q43204 is abundant in green tissues, rare in roots
 CC and leaves, and is about three-fold more abundant in leaf than that
 CC of Q43202. R37592 and R37593 show and overall homology of approx.
 CC 80%.

SO Sequence 446 AA;

Query Match 27.2%; Score 103; DB 7; Length 446;
 Best Local Similarity 100.0%; Pred. No. 7, 36e-163;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 lpyvlnvmldfvtlylhhghedklypyrgkewylrglttdrtygltnhhhtgch 366
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 239 lryvlnvmldfvtlylhhghedklypyrgkewylrglttdrtygltnhhhtgch 298
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 367 vlhhlfpqlyhyhlveateakpvlgykyrepdsgplrhll 409
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 299 vlnhlfpoiprhylhvaeateakpvlgykyrepdsgplrhll 341
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 5
 ID R60500 standard; Protein: 435 AA.

AC R60500;
 DT 28-MAR-1995 (first entry)
 DE Linoleic acid desaturase fad6.
 KW Linoleic acid desaturase; fad6; transgenic plant; crop improvement;
 KM Linoleic acid.
 OS Arabidopsis.
 PN MO9418337-A.
 PD 18-AUG-1994.
 PF 04-FEB-1994; U01321.
 PR 05-FEB-1993; US-014431.
 PR 22-NOV-1993; US-156551.
 PA (MONS) MONSANTO CO.
 PI (UNMS) UNIV MICHIGAN STATE.
 PI Aronold VZD, Gibson ST, Kishore GM, Ruif TG, Somerville CR;
 DR WPI: 94-279768/34.
 DR N-PSDB; Q71211.
 PT Genetically transformed plants with altered linoleic acid
 PT content - conty recombinant, double-stranded DNA encoding
 PT linoleic acid desaturase, or the antisense of the coding
 PT sequence
 PS Disclosure; Page 79-81; 144pp; English.
 CC The cDNA sequence and deduced amino acid sequence of linoleic-
 CC acid-desaturase fad6 of Arabidopsis are provided.

Query Match 11.4%; Score 43; DB 11; Length 435;
 Best Local Similarity 100.0%; Pred. No. 6, 52e-57;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 lnnlhhdigtlyhlhlfqlyhyhlveateakpvlgykyrep 391
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 288 lnnlhhdigtlyhlhlfqlyhyhlveateakpvlgykyrep 330
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 6
 ID W13381 standard; Protein: 447 AA.

AC W13381;
 DT 02-DEC-1997 (first entry)
 DE Sesame omega-3 aliphatic acid desaturase.
 KW Sesame; omega-3 aliphatic acid desaturase; modify; fat; oil; plant;
 KM Linoleic acid; recombinant production.
 OS Sesamum indicum.
 PN J09065882-A.
 PD 11-MAR-1997.
 PR 01-SEP-1995; 225145.
 PR 01-SEP-1995; JP-225145.
 PA (TOYA-) TOYAMA KEN.
 DR WPI: 97-220417/20.
 DR N-PSDB; T62066.
 PT Sesame omega-3 aliphatic acid desaturase gene - useful in genetic
 PT engineering to modify fats and oils in agricultural products
 PS Claim 6; Page 4; 10pp; Japanese.
 CC This protein is a sesame omega-3 aliphatic acid desaturase. Its coding
 CC sequence can be used in genetic engineering to modify fats and oils in
 CC agricultural products. The gene or enzyme can be introduced into a plant
 CC to modify the aliphatic acid composition in its oils and fats, to give
 CC oils and fats with a high content of linoleic acid. Antisense DNA can
 CC be introduced into a plant to inhibit the expression of the gene, so
 CC that oils and fats with little or no linoleic acid are produced. The
 CC gene can also be expressed in microorganisms for recombinant production
 CC the enzyme.

SO Sequence 447 AA;

Query Match 9.5%; Score 36; DB 24; Length 447;
 Best Local Similarity 100.0%; Pred. No. 6, 44e-45;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 323 vylhghghedklypyrgkewylrglttdrtygl 358
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 251 vylhghghedklypyrgkewylrglttdrtygl 286
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 7

ID R37596 standard; Protein: 453 AA.

AC R37596;
 DT 01-OCT-1993 (first entry)
 DE Sequence of soybean plastid delta-15 desaturase.
 KW Lipid composition; modification; fatty acid desaturase; enzyme.
 OS Glycine max, clone pSFD-118bp.
 PN MO9311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB; Q43208.
 PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure; Page 148-150; 167pp; English.
 CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15

CC desaturase cDNA was used as a hybridization probe to isolate a
CC glycerolipid desaturase cDNA from soybean. Plasmid pXf1 was
CC deposited under ATCC 68874. Soybean microsomal delta-15
CC desaturase cDNA was used as a hybridization probe to isolate cDNAs
CC encoding related desaturases from soybean. The insert of
CC pSPD-11bwp contained a stretch of 1675 nucleotides which contained
CC an open-reading frame encoding a polypeptide (R37596) of about
CC 80% identity with, and colinear with, the Arabidopsis plastid
CC delta-15 desaturase polypeptide listed in R37593. Nucleotides 169
CC to 382 encode the putative plastid transit peptide, colinear with
CC and sharing some homology with the transit peptide described for
CC the Arabidopsis plastid delta-15 glycerolipid desaturase (R37593).
SQ Sequence 453 AA;

Query Match 9.5%; Score 36; DB 7; Length 453;
Best Local Similarity 100.0%; Pred. No. 6.44e-45;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 vtylhhghedk1pwyrgkwsy1rgglttldtdyg 362
|
OY 251 VTYLHHGHEDKLPWYRGKWSYLRGGLTTLDRDYG 286

RESULT 8
ID R37598 standard; Protein; 156 AA.
AC R37598;
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone Pfadx-2 and Pfacp7.
PN M09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS; 93-197063/24.
DR WPI; 93-197063/24.
N-PSDB; Q43210.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 155; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q4324. Q43210 is the partial
CC composite sequence derived from the inserts in plasmids Pfadx-2 and
CC Pfacp7. R37598 is a deduced partial peptide sequence of its ORF.
SQ Sequence 156 AA;

Query Match 7.9%; Score 30; DB 7; Length 156;
Best Local Similarity 100.0%; Pred. No. 8.83e-35;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 95 aggtmfwalfv1ghdcgshfsndprlnsv 124
|
OY 82 AOGTMEWALFVLGHDCGSHFSNDPRLNSV 111

RESULT 9
ID R60498 standard; Protein; 383 AA.
AC R60498;
DT 28-MAR-1995 (first entry)
DE linoleic-acid-desaturase; fad3;
KW linoleic-acid-desaturase; fad3; oilseed rape; rapeseed;
KW transgenic plant; crop improvement; yeast artificial chromosome;

KW YAC; linoleic acid.
OS Brassica napus.
PN W09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PA (UNMS) UNIV MICHIGAN STATE.
PI Ardelon VJ, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
DR WPI; 94-279758/34.
N-PSDB; Q71203.
PT Genetically transformed plants with altered linoleic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoleic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 69-71; 144pp; English.
CC cDNA encoding the linoleic-acid-desaturase (fad3) of B. napus was
CC isolated from a YAC library using RFLP 220 and ASA2 markers as
CC probes. Isolated DNA was amplified using the primers given in
CC Q71204-09, and used to screen YAC libraries. The fad3 gene was
CC identified in YAC EW7D11.
SQ Sequence 383 AA;

Query Match 7.4%; Score 28; DB 11; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.93e-31;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 llvpyhgwrishtbqhghvndesw 150
|
OY 120 llvpyhgwrishtbqhghvndesw 147

RESULT 10
ID R37592 standard; Protein; 386 AA.
AC R37592;
DT 01-OCT-1993 (first entry)
DE Sequence of delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone pCF3.
PN M09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS; 93-197063/24.
DR WPI; 93-197063/24.
N-PSDB; Q43202.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 127-129; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224.
SQ Sequence 386 AA;

Query Match 7.4%; Score 28; DB 7; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.93e-31;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 llvpyhgwrishtbqhghvndesw 153
|
OY 120 llvpyhgwrishtbqhghvndesw 147

RESULT 11
ID R37595 standard; Protein: 380 AA.
AC R37595;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 desaturase,
KM Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pXf1.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992: U10284.
PR 04-DEC-1991: US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: 043207.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 144-146; 167pp; English.
CC PCR3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCR3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15
CC desaturase cDNA was used as a hybridization probe to isolate a
CC glycerolipid desaturase cDNA from soybean. Plasmid pXf1 was
CC deposited under ATCC 68874.
SQ Sequence 380 AA;

Query Match 7.1%; Score 27; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 8.83e-30;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 295 nbbdthvthhlfqqlphylveat 321
|||
QY 290 NHHDHGTHVHLEPQPHYLVEAT 316

RESULT 12
ID R37597 standard; Protein: 126 AA.
AC R37597;
DT 01-OCT-1993 (first entry)
DE Sequence of an internal region of a corn seed delta-15
DE desaturase.
KM Lipid composition; modification; fatty acid desaturase; enzyme.
OS Zea mays; clone pPCR20.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992: U10284.
PR 04-DEC-1991: US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: 043209.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 152-153; 167pp; English.
CC PCR3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCR3
CC insert was also used. The identity of the expression product of PCR3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of

CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Q43209 is the
CC complete nucleotide sequence of a 396 bp polymerase chain reaction
CC product derived from corn seed mRNA that is found in the insert of
CC plasmid pPCR20. Nucleotides 1 to 31 and 364 to 396 correspond to
CC the amplification primers described in Q43211 and Q43212
CC respectively. Nucleotides 31 to 363 encode a region that is 61.9%
CC identical to the region between amino acids 137 and 249 of R37591.
SQ Sequence 126 AA;

Query Match 2.4%; Score 9; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 5.61e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 118 vtylhhgh 126
|||
QY 251 VTYLHHRGH 259

RESULT 13
ID R53700 standard; Protein: 387 AA.
AC R53700;
DT 09-NOV-1994 (first entry)
DE Sequence of corn microsomal delta-12 desaturase deduced from the
DE cDNA in plasmid pFad2 1.
KM Fatty acid; desaturase; lipid; unsaturated; transgenic plant.
OS Zea mays.
PN W09411516-A.
PD 26-MAY-1994.
PF 15-OCT-1993: U09987.
PR 17-NOV-1992: US-977339.
PA (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Lightner JE, Okuley JJ;
DR WPI: 94-183515/22.
DR N-PSDB: Q66071.
PT Genes for fatty acid desaturase enzymes - permit alteration of
PT plant lipid composition
PS Claim 13; Page 124-126; 147pp; English.
CC Corn microsomal delta-12 desaturase cDNA was isolated using a PCR
CC approach. A cDNA library was made to poly A+ mRNA from developing
CC corn embryos. This library was used as template for PCR using sets
CC of degenerate oligos NS3 (Q66075) and RB5A/B (Q66077, Q66078) as
CC sense and antisense primers, respectively. NS3 and RB5A/B corresp.
CC to stretches of AAs 101-109 and 318-326, respectively, of R53697,
CC which are conserved in most microsomal delta-12 desaturases. A PCR
CC product of 720bp was purified and used as a probe for screening the
CC corn cDNA library. A plaque was purified and found to encode
CC microsomal delta-12 desaturase truncated at the 3' end. This cDNA
CC was used to probe the corn cDNA library again. The clone contg.
CC (Q66071). An isolated nucleic acid fragment
CC wherein the nucleic acid identity is 90% or greater to
CC Q66071 is claimed. A method to isolate nucleic acid fragments
CC encoding fatty acid desaturases and related enzymes is claimed
CC which comprises: comparing AA sequences in R53697-R53702 and other
CC fatty acid desaturase sequences; identifying conserved sequences of
CC 4 or more AAs; designing degenerate oligos based on the conserved
CC sequences; and using the oligos to isolate sequences encoding fatty
CC acid desaturases and desaturase-related enzymes.
SQ Sequence 387 AA;

Query Match 2.4%; Score 9; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 5.61e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 92 wplywiag 100
|||
QY 76 WPLYWIAG 84

RESULT 14
ID R80294 standard; Protein: 20 AA.

AC R80294: (first entry)
DE 19-JAN-1996 (first entry)
DE Trehalose releasing enzyme N-terminal fragment.
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriose; alpha-maltotetraose; alpha-maltopentaose;
KW maltopentaoxyltrehalose; maltopentaoxyltrehalose; maltopentaoxyltrehalose;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
OS Archaeobacter sp. Q36.
PN EP-671470-A2.
PD 13-SEP-1995.
PF 07-MAR-1995: 301474.
PR 07-MAR-1994: JP-059840.
PR 07-MAR-1994: JP-059834.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
DR WPI: 95-312772/41.
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
PT from a non-reducing saccharide having a trehalose structure as an
PT end unit.
PS Example 4; Page 25; 45pp; English.
CC The trehalose releasing enzyme can be used for the preparation of
CC trehalose with high yields and efficiency from non-reducing
CC saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriose, alpha-maltotetraose, alpha-maltopentaose and
CC maltopentaoxyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
CC This is the N-terminal sequence of the enzyme.
SQ Sequence 20 AA:

Query Match 2.1%; Score 8; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.08e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 7 eaakpvlg 14
|||||||
QY 317 EAKPVLG 324

RESULT 15
ID R80290 standard; Protein; 597 AA.
AC R80290:
DE 19-JAN-1996 (first entry)
DE Trehalose releasing enzyme.
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriose; alpha-maltotetraose; alpha-maltopentaose;
KW maltopentaoxyltrehalose; maltopentaoxyltrehalose; maltopentaoxyltrehalose;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
OS Archaeobacter sp. Q36.
PN EP-671470-A2.
PD 13-SEP-1995.
PF 07-MAR-1995: 301474.
PR 07-MAR-1994: JP-059840.
PR 07-MAR-1994: JP-059834.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
DR WPI: 95-312772/41.
DR N-PSDB: 098670.
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
PT from a non-reducing saccharide having a trehalose structure as an
PT end unit.
PS Claim 3; Page 24-25; 45pp; English.
CC This enzyme can be used for the preparation of trehalose with high
CC yields and efficiency from non-reducing saccharides such as
CC alpha-glucosyltrehalose, alpha-maltosyltrehalose, alpha-maltotriose,
CC alpha-maltotetraose, alpha-maltopentaose and maltopentaoxyltrehalose.
CC The trehalose can be used as a sweetener, taste-improving agent,
CC quality-improving agent, stabiliser, filler, excipient or adjuvant in food products cosmetics and pharmaceuticals.
SQ Sequence 597 AA:

Query Match 2.1%; Score 8; DB 14; Length 597;
Best Local Similarity 100.0%; Pred. No. 1.08e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 7 eaakpvlg 14
|||||||
QY 317 EAKPVLG 324

Search completed: Sat Aug 21 12:22:23 1999
Job time : 246 secs.

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W E I R E (TM)

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Msearch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:26:29 1999; Maspar time 4.93 Seconds

Tabular output not generated. 777.764 Million cell updates/sec

Title: >US09-219-935-7

Description: (1-378) from US09219935.pep

Sequence: 1 LTVDSSSPPIEEPKTORF.....DVYYEADPNLGEIKVTAE 378

Scoring table: TABLE UNIPROTABLE
Gap 60

Searched: 106580 segs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: 2-issued
US09-219-935-7

Statistics: Mean 2.741; Variance 0.681; scale 4.025

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	378	100.0	378	3	PCT-US92-1 Sequence 7, Applicatio	0.00e+00
2	378	100.0	404	3	PCT-US92-1 Sequence 9, Applicatio	0.00e+00
3	103	27.2	446	3	PCT-US94-0 Sequence 10, Applicati	4.67e-156
4	103	27.2	446	3	PCT-US92-1 Sequence 5, Applicati	4.67e-156
5	43	11.4	435	3	PCT-US94-0 Sequence 12, Applicati	5.66e-43
6	36	9.5	453	3	PCT-US92-1 Sequence 13, Applicati	1.66e-43
7	31	8.2	156	3	PCT-US92-1 Sequence 17, Applicati	2.06e-35
8	28	7.4	383	3	PCT-US94-0 Sequence 2, Applicatio	1.31e-30
9	28	7.4	386	3	PCT-US92-1 Sequence 2, Applicatio	1.31e-30
10	27	7.1	380	3	PCT-US92-1 Sequence 11, Applicati	5.11e-29
11	25	6.6	37	2	US-08-320- Sequence 6, Applicatio	7.46e-26
12	25	6.6	37	2	US-08-320- Sequence 22, Applicati	7.46e-26
13	25	6.6	37	1	US-08-314- Sequence 6, Applicatio	7.46e-26
14	25	6.6	37	1	US-08-314- Sequence 22, Applicati	7.46e-26
15	22	5.8	37	1	US-08-314- Sequence 16, Applicati	3.68e-21
16	22	5.8	37	1	US-08-314- Sequence 12, Applicati	3.68e-21
17	22	5.8	37	2	US-08-320- Sequence 16, Applicati	3.68e-21
18	22	5.8	37	2	US-08-320- Sequence 12, Applicati	3.68e-21
19	18	4.8	40	2	US-08-320- Sequence 10, Applicati	4.96e-15
20	18	4.8	40	2	US-08-320- Sequence 18, Applicati	4.96e-15
21	18	4.8	40	1	US-08-314- Sequence 10, Applicati	4.96e-15
22	18	4.8	40	1	US-08-314- Sequence 18, Applicati	4.96e-15
23	12	3.2	37	1	US-08-314- Sequence 26, Applicati	2.82e-06

ALIGNMENTS

RESULT ID	1	STANDARD	PRT	378 AA.
XX	PCT-US92-10284-7			
XX	xxxxxx			
XX				
DE	Sequence 7, Application PC/TUS9210284			
CC	Sequence 7, Application PC/TUS9210284			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Browne, John, Kinney, Anthony J.,			
CC	APPLICANT: Pierce, John, Wierzbicki, Anna M.,			
CC	APPLICANT: Yadav, Narendra S., Perez-Grau, Luis			
CC	TITLE OF INVENTION: Fatty Acid Desaturase Genes			
CC	NUMBER OF SEQUENCES: 32			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: E. I. du Pont de Nemours and Company			
CC	STREET: 1007 Market Street			
CC	CITY: Wilmington			
CC	STATE: Delaware			
CC	COUNTRY: U.S.A.			
CC	ZIP: 19898			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: Macintosh			
CC	OPERATING SYSTEM: Macintosh System, 6.0			
CC	SOFTWARE: Microsoft Word, 4.0			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: PCT/US92/10284			
CC	FILING DATE: 19921203			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: 07/804,259			
CC	FILING DATE: 4 DECEMBER 1991			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Floyd, Linda A.			
CC	REGISTRATION NUMBER: 33,692			
CC	REFERENCE/DOCKET NUMBER: BB-1036-A			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (302) 992-4929			
CC	TELEFAX: (302) 892-7949			
CC	TELEX: 835420			
CC	INFORMATION FOR SEQ ID NO: 7:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 378 amino acids			

CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 378 AA; 43528 MW; 793455 CN;

Query Match 100.0%; Score 378; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 LTVDSSSSPPIEEBKTRQFDPGAPPPNLAIDIRAIPKHCWKNPKMSYVYRELAIY 60
OY 1 LTVDSSSSPPIEEBKTRQFDPGAPPPNLAIDIRAIPKHCWKNPKMSYVYRELAIY 60
Db 61 FALAAGAAIYLNMLVWPPIYIAOQTMFVALFVLGHDGCHGSFSDPRLNSVGHLLHSSI 120
OY 61 FALAAGAAIYLNMLVWPPIYIAOQTMFVALFVLGHDGCHGSFSDPRLNSVGHLLHSSI 120
Db 121 LVPYHGRIISRTHHONHGHVENDSWHPMSSEKIKSLDKPTFRFRFTLPVLMAYPFYL 180
OY 121 LVPYHGRIISRTHHONHGHVENDSWHPMSSEKIKSLDKPTFRFRFTLPVLMAYPFYL 180
Db 181 WARSFGKGSYHHPDSDLFLPKERNVDLTSTACWTAMAVLLVCNLFVGMQMLKLYIIP 240
OY 181 WARSFGKGSYHHPDSDLFLPKERNVDLTSTACWTAMAVLLVCNLFVGMQMLKLYIIP 240
Db 241 YWINVMMLDFVTYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIHHDIGTHVI 300
OY 241 YWINVMMLDFVTYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIHHDIGTHVI 300
Db 301 HHLFPOIPHYHLVETEAAPKPVLGKYYREPDKSGPLPLHLGLIAKSIKEDHFVSDEGDV 360
OY 301 HHLFPOIPHYHLVETEAAPKPVLGKYYREPDKSGPLPLHLGLIAKSIKEDHFVSDEGDV 360
Db 361 VYVEADPNLYGEIKVTAE 378
OY 361 VYVEADPNLYGEIKVTAE 378

RESULT 2 STANDARD; PRT; 404 AA.
ID PCT-US92-10284-9
XX xxxxxx
AC
XX
DT
XX
DE Sequence 9, Application PC/TUS9210284
XX
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yaday, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259

CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 404 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 404 AA; 46617 MW; 906055 CN;

Query Match 100.0%; Score 378; DB 3; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 LTVDSSSSPPIEEBKTRQFDPGAPPPNLAIDIRAIPKHCWKNPKMSYVYRELAIY 86
OY 1 LTVDSSSSPPIEEBKTRQFDPGAPPPNLAIDIRAIPKHCWKNPKMSYVYRELAIY 60
Db 87 FALAAGAAIYLNMLVWPPIYIAOQTMFVALFVLGHDGCHGSFSDPRLNSVGHLLHSSI 146
OY 61 FALAAGAAIYLNMLVWPPIYIAOQTMFVALFVLGHDGCHGSFSDPRLNSVGHLLHSSI 120
Db 147 LVPYHGRIISRTHHONHGHVENDSWHPMSSEKIKSLDKPTFRFRFTLPVLMAYPFYL 206
OY 121 LVPYHGRIISRTHHONHGHVENDSWHPMSSEKIKSLDKPTFRFRFTLPVLMAYPFYL 180
Db 207 WARSFGKGSYHHPDSDLFLPKERNVDLTSTACWTAMAVLLVCNLFVGMQMLKLYIIP 266
OY 181 WARSFGKGSYHHPDSDLFLPKERNVDLTSTACWTAMAVLLVCNLFVGMQMLKLYIIP 240
Db 267 YWINVMMLDFVTYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIHHDIGTHVI 326
OY 241 YWINVMMLDFVTYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIHHDIGTHVI 300
Db 327 HHLFPOIPHYHLVETEAAPKPVLGKYYREPDKSGPLPLHLGLIAKSIKEDHFVSDEGDV 386
OY 301 HHLFPOIPHYHLVETEAAPKPVLGKYYREPDKSGPLPLHLGLIAKSIKEDHFVSDEGDV 360
Db 387 VYVEADPNLYGEIKVTAE 404
OY 361 VYVEADPNLYGEIKVTAE 378

RESULT 3 STANDARD; PRT; 446 AA.
ID PCT-US94-01321-10
XX xxxxxx
AC
XX
DT
XX
DE Sequence 10, Application PC/TUS9401321
XX
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
CC TITLE OF INVENTION: in Plants
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994

CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 446 AA; 51174 MW; 1094717 CN;
SQ

Query Match 27.2%; Score 103; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 4.67e-156;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPWINVMWLDFTVYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHDIGTH 366
|||
Qy 239 IPWINVMWLDFTVYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHDIGTH 298
|||

Db 367 VIHHLFPOIPHYHLVEATEAKPVLGKYRPPDKSGPLPHLL 409
|||
Qy 299 VIHHLFPOIPHYHLVEATEAKPVLGKYRPPDKSGPLPHLL 341
|||

RESULT 4
ID PCT-US92-10284-5 STANDARD; PRT; 446 AA.
XX
AC xxxxxx
XX
DT
XX

Sequence 5, Application PC/TUS9210284
GENERAL INFORMATION:
CC APPLICANT: Brower, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 5:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 446 AA; 51174 MW; 1094717 CN;
SQ

Query Match 27.2%; Score 103; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 4.67e-156;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPWINVMWLDFTVYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHDIGTH 366
|||
Qy 239 IPWINVMWLDFTVYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHDIGTH 298
|||

Db 367 VIHHLFPOIPHYHLVEATEAKPVLGKYRPPDKSGPLPHLL 409
|||
Qy 299 VIHHLFPOIPHYHLVEATEAKPVLGKYRPPDKSGPLPHLL 341
|||

RESULT 5
ID PCT-US94-01321-12 STANDARD; PRT; 435 AA.
XX
AC xxxxxx
XX
DT
XX

Sequence 12, Application PC/TUS9401321
GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 435 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 435 AA; 50136 MW; 1054240 CN;
SQ

Query Match 11.4%; Score 43; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 5.67e-55;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 INNHHHDIGTHVHHLFPOIPHYHLVEATEAKPVLGKYREP 391
|||
Qy 288 INNHHHDIGTHVHHLFPOIPHYHLVEATEAKPVLGKYREP 330
|||

RESULT 6
ID PCT-US92-10284-13 STANDARD; PRT; 453 AA.
XX
AC xxxxxx
XX
DT

XX Sequence 13, Application PC/TUS9210284
DE
XX
CC Sequence 13, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadev, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 453 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 453 AA; 51362 MW; 1146882 CN;
SQ
Query Match 9.5%; Score 36; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.66e-43;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 327 VTYLHHGHGDKLPWYRGKESYLRGGLTTLDRDYG 362
QY 251 VTYLHHGHGDKLPWYRGKESYLRGGLTTLDRDYG 286
RESULT 7
ID PCT-US92-10284-17 STANDARD: PRT; 156 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 17, Application PC/TUS9210284
XX
CC Sequence 17, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadev, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC

CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: Macintosh
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: YES
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Arabidopsis thaliana
CC IMMEDIATE SOURCE:
CC CLONE: pFadk-2 and pYacp7
CC SEQUENCE 156 AA; 17771 MW; 128823 CN;
SQ
Query Match 8.2%; Score 31; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.06e-35;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 126 GHLSHSILVYHGWRIHSRTHHONGHVEN 156
QY 113 GHLSHSILVYHGWRIHSRTHHONGHVEN 143
RESULT 8
ID PCT-US94-01321-2 STANDARD: PRT; 383 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 2, Application PC/TUS9401321
XX
CC Sequence 2, Application PC/TUS9401321
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
CC TITLE OF INVENTION: in Plants
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PC-DOS/MS-DOS
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994
CC

CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 383 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC SEQUENCE 383 AA; 43936 MW; 846574 CN;
SQ

Query Match 7.4%; Score 28; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.31e-30;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 ILVPHGMRIHRTTHQNHGVNDESM 150
120 ILVPHGMRIHRTTHQNHGVNDESM 147
|||||

RESULT 9
ID PCT-US92-10284-2 STANDARD; PRT; 386 AA.
XX xxxxxx
XX

Sequence 2, Application PC/TUS9210284

CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 386 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear

CC MOLECULE TYPE: protein
SQ SEQUENCE 386 AA; 44076 MW; 854247 CN;
SQ

Query Match 7.4%; Score 28; DB 3; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.31e-30;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 ILVPHGMRIHRTTHQNHGVNDESM 153
120 ILVPHGMRIHRTTHQNHGVNDESM 147
|||||

RESULT 10
ID PCT-US92-10284-11 STANDARD; PRT; 380 AA.
XX xxxxxx
XX

Sequence 11, Application PC/TUS9210284

CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 380 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 380 AA; 44185 MW; 827651 CN;
SQ

Query Match 7.1%; Score 27; DB 3; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.11e-29;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 295 NIHHDIGTHVYHHLFPOIPHYHVEAT 321
QY 290 NIHHDIGTHVYHHLFPOIPHYHVEAT 316
|||||

RESULT 11
ID US-08-320-982-6 STANDARD; PRT; 37 AA.
AC xxxxxx
XX
DT
XX
DE Sequence 6, Application US/08320982
XX
CC Sequence 6, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KORULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;
SQ
Query Match 6.6%; Score 25; DB 2; length 37;
Best Local Similarity 100.0%; Pred. No. 7.46e-26;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHDIQTHVHHLFPOIPHYHLEAT 25
|||
QY 292 HHDIQTHVHHLFPOIPHYHLEAT 316
RESULT 12
ID US-08-320-982-22 STANDARD; PRT; 37 AA.
AC xxxxxx
XX
DT
XX
DE Sequence 22, Application US/08320982
XX
CC Sequence 22, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:

CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KORULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;
SQ
Query Match 6.6%; Score 25; DB 2; length 37;
Best Local Similarity 100.0%; Pred. No. 7.46e-26;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHDIQTHVHHLFPOIPHYHLEAT 25
|||
QY 292 HHDIQTHVHHLFPOIPHYHLEAT 316
RESULT 13
ID US-08-314-596-6 STANDARD; PRT; 37 AA.
AC xxxxxx
XX
DT
XX
DE Sequence 6, Application US/08314596
XX
CC Sequence 6, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA: 4331 MW: 8403 CN;
SQ

Query Match 6.6%; Score 25; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 7,466-26;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDTGTHVHHLFPOIPHYHLVEAT 25
OY 292 HHDTGTHVHHLFPOIPHYHLVEAT 316
|||||

RESULT 14
ID US-08-314-596-22 STANDARD: PRT; 37 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 22, Application US/08314596
XX
CC Sequence 22, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DABRY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000

CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA: 4331 MW: 8403 CN;
SQ

Query Match 6.6%; Score 25; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 7,466-26;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDTGTHVHHLFPOIPHYHLVEAT 25
OY 292 HHDTGTHVHHLFPOIPHYHLVEAT 316
|||||

RESULT 15
ID US-08-314-596-16 STANDARD: PRT; 37 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 16, Application US/08314596
XX
CC Sequence 16, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DABRY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA: 4407 MW: 7119 CN;
SQ

Query Match 5.8%; Score 22; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 3,686-21;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDTGTHVHHLFPOIPHYHLV 22

|||||
Qy 292 HHDI GTV I H L P Q I P H Y H L V 313

Search completed: Sat Aug 21 12:26:46 1999
Job time : 17 secs.



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NWSEH (TM)

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Msearch - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:31:25 1999; Maspar time 16.73 Seconds
Tabular output not generated. 967.513 Million cell updates/sec

Title: >US-09-219-935-9
Description: (1-404) from US09219935.pep
Perfect Score: 404
Sequence: 1 FKFQSPSPFRFLNSRNMA.....DVYYEADPNLGEIKVTAE 404

Scoring table: TABLE uniprottable
Gap 60

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr60
1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 3.655; Variance 0.462; scale 7.903

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	404	100.0	404	2	P00812	omega-3 fatty acid de
2	103	25.5	446	2	J02336	omega-3 fatty acid de
3	43	10.6	398	2	T01696	omega-3 fatty acid de
4	40	9.9	441	2	T03029	omega-3 fatty acid de
5	36	8.9	443	2	T01697	omega-3 fatty acid de
6	36	8.9	453	2	J02339	omega-3 fatty acid de
7	28	6.9	377	2	J02337	omega-3 fatty acid de
8	28	6.9	383	2	A44227	omega-3 fatty acid de
9	28	6.9	386	2	J02335	omega-3 fatty acid de
10	27	6.7	380	2	J02338	omega-3 fatty acid de
11	24	5.9	379	2	J02555	omega-3 fatty acid de
12	16	4.0	359	2	S52650	omega-3 fatty acid de
13	13	2.0	226	2	H71349	probable ribosomal pr
14	14	2.0	598	2	S65770	maltooligosyltrehalos
15	15	2.0	1117	2	S63399	probable membrane pro
16	7	1.7	112	2	A25458	neuropeptide L5 precu
17	7	1.7	113	2	A60887	synuclein - Pacific e
18	7	1.7	213	2	S08313	abscisic acid-induced
19	7	1.7	224	2	S16259	embryonic abundant pr
20	7	1.7	232	2	D70754	hypothetical protein
21	7	1.7	249	2	S78186	H+-transporting ATP s
22	7	1.7	299	2	T00774	hypothetical protein
23	7	1.7	305	2	A70212	conserved hypothetical

24	7	1.7	317	2	S55316	mucin (clone PGM-2B)	4.35e+00
25	7	1.7	337	2	A54214	pentanene synthase	4.35e+00
26	7	1.7	338	2	F69437	hypothetical protein	4.35e+00
27	7	1.7	342	2	E70463	conserved hypothetical	4.35e+00
28	7	1.7	367	1	W0H0	alpha-2-HS-glycoprote	4.35e+00
29	7	1.7	371	1	J06186	transcription factor	4.35e+00
30	7	1.7	388	2	F72995	alanine racemase (EC	4.35e+00
31	7	1.7	392	2	F69536	conserved hypothetical	4.35e+00
32	7	1.7	415	1	A30100	serine proteinase eas	4.35e+00
33	7	1.7	415	1	C64473	adenosylhomocysteinase	4.35e+00
34	7	1.7	447	2	B64495	hypothetical protein	4.35e+00
35	7	1.7	488	1	Q0BHS	alkaline exonuclease	4.35e+00
36	7	1.7	528	2	T01535	gastric mucin (clone	4.35e+00
37	7	1.7	553	2	T01535	probable cytochrome P	4.35e+00
38	7	1.7	555	2	I51671	Weila kinase - Africa	4.35e+00
39	7	1.7	674	2	S54091	hypothetical protein	4.35e+00
40	7	1.7	674	2	S75662	sensory transduction	4.35e+00
41	7	1.7	755	2	B41836	amine oxidase (flavin	4.35e+00
42	7	1.7	1065	2	B69795	acriflavin resistance	4.35e+00
43	7	1.7	1132	2	S37932	hypothetical protein	4.35e+00
44	7	1.7	1944	2	A55117	tsq24 protein - mouse	4.35e+00
45	7	1.7	2038	2	A43742	female sterile homeot	4.35e+00

ALIGNMENTS

RESULT 1
ENTRY P00812 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BND - rape
ORGANISM #formal_name Brassica napus #common_name rape
DATE 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999

ACCESSIONS P00812
REFERENCE J02335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references M01D:94302147
#contents CDNA:BND
#accession P00812
#molecule_type mRNA
#residues 1-404 #label YAD
##cross-references GB:I22963

COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 404 #molecular-weight 46617 #checksum 9400

Query Match 100.0%; Score 404; DB 2; Length 404;
Best local similarity 100.0%; Pred. No. 0.00e+00;

Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	EKFQSPSPFRFLNSRNMA	NTPTLVDS	SSSPTEEP	PKTORF	PGAP	PNFNL	ADIR	60
Qy	1	EKFQSPSPFRFLNSRNMA	LVNTPTLV	DS	SSSPTEEP	PKTORF	PGAP	PNFNL	ADIR
Qy	1	EKFQSPSPFRFLNSRNMA	LVNTPTLV	DS	SSSPTEEP	PKTORF	PGAP	PNFNL	ADIR
Db	61	AAIPKHCWVKNPKMSKYV	RELAIY	PALAGA	AYLN	NMTLV	WPLY	TAOCT	MFALFV
Qy	61	AAIPKHCWVKNPKMSKYV	RELAIY	PALAGA	AYLN	NMTLV	WPLY	TAOCT	MFALFV
Qy	61	AAIPKHCWVKNPKMSKYV	RELAIY	PALAGA	AYLN	NMTLV	WPLY	TAOCT	MFALFV
Db	121	HDGCHGSEFSDNPR	NSVGHLL	SSILV	PHGMR	ISRT	HHON	GHEN	ESMHPN
Qy	121	HDGCHGSEFSDNPR	NSVGHLL	SSILV	PHGMR	ISRT	HHON	GHEN	ESMHPN
Qy	121	HDGCHGSEFSDNPR	NSVGHLL	SSILV	PHGMR	ISRT	HHON	GHEN	ESMHPN
Db	181	YKSIDKPTREFRFTL	PLVMLA	YPFY	LWARS	PGKGS	HYH	PDSD	FLPK
Qy	181	YKSIDKPTREFRFTL	PLVMLA	YPFY	LWARS	PGKGS	HYH	PDSD	FLPK
Qy	181	YKSIDKPTREFRFTL	PLVMLA	YPFY	LWARS	PGKGS	HYH	PDSD	FLPK

Db 241 TAMAVLVCLNFVWGPOMKLYIPYINVMWIDFVYLLHHGHEDKLPYRGKMSYL 300
OY 241 TAMAVLVCLNFVWGPOMKLYIPYINVMWIDFVYLLHHGHEDKLPYRGKMSYL 300
Db 301 RGLTLDRODGLNNHHIDGTHVHLLFPQIPHYHLVTEAKPVLGKYRPPDSSG 360
OY 301 RGLTLDRODGLNNHHIDGTHVHLLFPQIPHYHLVTEAKPVLGKYRPPDSSG 360
Db 361 PLPLHLGLLAKSIKEDHFVSDGVDVYVYEAADPNLYGEIKYTAE 404
OY 361 PLPLHLGLLAKSIKEDHFVSDGVDVYVYEAADPNLYGEIKYTAE 404

RESULT 2
ENTRY J02336 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CFD -
ORGANISM Arabidopsis thaliana #common_name mouse-ear
#formal_name Arabidopsis thaliana #common_name mouse-ear
#status
#accession 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999
ACCESSIONS J02336; A49503
REFERENCE J02335
#authors Iadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Pelter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Rietter, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession J02336
#molecule_type mRNA
#residues 1-446 #label YAD

REFERENCE A49503
#authors Iba, K.; Gibson, S.; Nishituchi, T.; Fuse, T.; Nishimura, M.;
Arondel, V.; Hugly, S.; Somerville, C.
#journal J. Biol. Chem. (1993) 268:24099-24105
#title A gene encoding a chloroplast omega-3 fatty acid desaturase
complements alterations in fatty acid desaturation and
chloroplast copy number of the fad7 mutant of Arabidopsis
thaliana.
#cross-references MUID:94043239
#accession A49503
#status Preliminary
#molecule_type DNA
#residues 1-446 #label IBA
#cross-references GB:D14007; NID:9461160; PID:d1003612; PID:9541653
#note sequence extracted from NCBI backbone (NCBIN:139485,
NCBIP:139486)

COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 446 #molecular-weight 51174 #checksum 4653

Query Match 25.5%; Score 103; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 2,64e-297;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPYWINVMWLDVYTLHHGHEDKLPYRGKMSYLRGLTLDRODGLNNHHIDGTH 366
OY 265 IPYWINVMWLDVYTLHHGHEDKLPYRGKMSYLRGLTLDRODGLNNHHIDGTH 324
Db 367 VIHHLEPQIPHYHLVTEAKPVLGKYRPPDSSGPLRLHL 409
OY 325 VIHHLEPQIPHYHLVTEAKPVLGKYRPPDSSGPLRLHL 367

RESULT 3

ENTRY T01696 #type fragment
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD8 - maize
ORGANISM (fragment)
#formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
19-Feb-1999
ACCESSIONS T01696
REFERENCE Z14400
#authors Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;
Kusano, T.
#journal Plant Mol. Biol. (1998) 36:297-306
#title Two maize genes encoding omega-3 fatty acid desaturase and
their differential expression to temperature.
#accession T01696
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-398 #label BER
#cross-references EMBL:D63953; NID:d1164452; PID:l023305
#experimental_source strain honey bantum

GENETICS
#gene FAD8
#keywords oxidoreductase
SUMMARY #length 398 #checksum 5580

Query Match 10.6%; Score 43; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 6,40e-102;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 EWSYLRGGLTLDRODGLNNHHIDGTHVHLLFPQIPHYHL 333
OY 296 EWSYLRGGLTLDRODGLNNHHIDGTHVHLLFPQIPHYHL 338

RESULT 4
ENTRY T03029 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - common
ORGANISM tobacco
#formal_name Nicotiana tabacum #common_name common tobacco
DATE 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
24-Mar-1999
ACCESSIONS T03029
REFERENCE Z14828
#authors Hamada, T.; Nishituchi, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Plant Cell Physiol. (1996) 37:606-611
#title CDNA cloning of a wounding-inducible gene encoding a plastid
omega-3 fatty acid desaturase from tobacco.
#accession T03029
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-441 #label HAM
#cross-references EMBL:D79979; NID:d1093316; PID:g1694625
#experimental_source cultivar SRI

GENETICS
#gene FAD7
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 441 #molecular-weight 50310 #checksum 6941

Query Match 9.9%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 1,70e-92;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 355 INNHHIDGTHVHLLFPQIPHYHLVTEAKPVLGKY 394
OY 314 INNHHIDGTHVHLLFPQIPHYHLVTEAKPVLGKY 353

RESULT 5
ENTRY T01697 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize
ORGANISM #formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
19-Feb-1999

ACCESSIONS T01697
REFERENCE Z14400
#authors Beberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;
#journal Kusano, T.
#title Plant Mol. Biol. (1998) 36:297-306
#accession T01697
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-443 ##label BER
#cross-references EMBL:D63954; NID:d1164453; PID:d1023306
#experimental_source strain honey bantam

GENETICS
#gene FAD7
#introns 163/2; 193/2; 215/3; 246/3; 308/3; 335/3; 381/3
#exons oxidoreductase
#length 443 #molecular-weight 49437 #checksum 8872

KEYWORDS
SUMMARY

Query Match 8.9%; Score 36; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 4.88e-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 317 VTYLHHGHEDKLPWYRGKESYLRGGLTTLDRDYG 352
OY 277 VTYLHHGHEDKLPWYRGKESYLRGGLTTLDRDYG 312

RESULT 6
ENTRY JQ2339
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean
ORIGIN #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

ACCESSIONS JQ2339
REFERENCE JQ2335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:GMD
#accession JQ2339
##molecule_type mRNA
##residues 1-453 ##label YAD
##cross-references GB:L22965; NID:9408791; PID:9408792
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 453 #molecular-weight 51362 #checksum 7549

Query Match 8.9%; Score 36; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.88e-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 VTYLHHGHEDKLPWYRGKESYLRGGLTTLDRDYG 362
OY 277 VTYLHHGHEDKLPWYRGKESYLRGGLTTLDRDYG 312

RESULT 7
ENTRY JQ2337
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BN3 - rape
ORIGIN #formal_name Brassica napus #common_name rape
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

ACCESSIONS JQ2337
REFERENCE JQ2335

#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:BN3
#accession JQ2337
##molecule_type mRNA
##residues 1-377 ##label YAD
##cross-references GB:L22962; NID:9408491; PID:9408492
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 377 #molecular-weight 43258 #checksum 3294

Query Match 6.9%; Score 28; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.31e-55;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 117 ILVYHGMRIISHRTHQNHGVNDESM 144
OY 146 ILVYHGMRIISHRTHQNHGVNDESM 173

RESULT 8
ENTRY A44227
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - rape
ORIGIN #formal_name Brassica napus #common_name rape
DATE 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

ACCESSIONS A44227
REFERENCE A44227
#authors Aronde, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman,
H.M.; Somerville, C.R.;
Science (1992) 258:1353-1355
#journal Map-based cloning of a gene controlling omega-3 fatty acid
desaturation in Arabidopsis.
#cross-references MUID:93088059
#accession A44227
##status Preliminary; not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-383 ##label ARO
##cross-references GB:L01418; NID:9167147; PID:9167148
COMMENT ##note sequence extracted from NCBI backbone (NCBI:119842)
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 383 #molecular-weight 43936 #checksum 2897

Query Match 6.9%; Score 28; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.31e-55;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 ILVYHGMRIISHRTHQNHGVNDESM 150
OY 146 ILVYHGMRIISHRTHQNHGVNDESM 173

RESULT 9
ENTRY JQ2335
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 -
Arabidopsis thaliana
ORIGIN #formal_name Arabidopsis thaliana #common_name mouse-ear
cress
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 12-Mar-1999

ACCESSIONS JQ2335;
REFERENCE T02487

REFERENCE J02335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references M01D:94302147
#accession J02335
#molecule_type mRNA
#residues 1-386 ##label YAD
REFERENCE J14675
#authors Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
J.C.
#submission Submitted to the EMBL Data Library, August 1998
#description Arabidopsis thaliana chromosome II BAC F23F1 genomic
sequence.
#accession T02487
#status Translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-386 ##label ROU
#cross-references EMBL:NC004680; NID:g3420043; PID:g3420053
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
GENETICS
#map_position II
#introns 103/2; 133/2; 155/3; 186/3; 248/3; 275/3; 321/3
#note F23F1.10
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 386 #molecular-weight 44076 #checksum 8044
Query Match 6.9%; Score 28; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.31e-55;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 126 ILVPHGWRISHRTHQNHGHNDESW 153
|||
QY 146 ILVPHGWRISHRTHQNHGHNDESW 173
RESULT 10
ENTRY J02338 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GM3 - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999
ACCESSIONS J02338
REFERENCE J02335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references M01D:94302147
#accession J02338
#molecule_type mRNA
#residues 1-380 ##label YAD
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase; transmembrane protein
SUMMARY #length 380 #molecular-weight 44185 #checksum 1659
Query Match 6.7%; Score 27; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.29e-52;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 295 NHHHDIGTHVHHLFPOIPHYHLEAT 321
|||
QY 316 NHHHDIGTHVHHLFPOIPHYHLEAT 342
RESULT 11
ENTRY JC2555 #type complete
TITLE omega-3 fatty acid desaturase - common tobacco (cv. SR1)
ORGANISM #formal_name Nicotiana tabacum #common_name common tobacco
DATE 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change
24-Sep-1998
ACCESSIONS JC2555
REFERENCE JC2555
#authors Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Gene (1994) 147:293-294
#title Cloning of a cDNA encoding tobacco omega-3 fatty acid
desaturase.
#cross-references M01D:95011632
#accession JC2555
#status Preliminary
#molecule_type mRNA
#residues 1-379 ##label HAM
#cross-references DBJ:D26509; NID:g1311480; PID:d1006059; PID:g599592
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
SUMMARY #length 379 #molecular-weight 44149 #checksum 1940
Query Match 5.9%; Score 24; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 9.77e-44;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 291 NHHHDIGTHVHHLFPOIPHYHL 314
|||
QY 315 NHHHDIGTHVHHLFPOIPHYHL 338
RESULT 12
ENTRY S52650 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - Synecocystis
sp. (strain PCC6803)
ALTERNATE_NAMES delta 15 desaturase
ORGANISM #formal_name Synecocystis sp.
#variety PCC 6803
DATE 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
17-Mar-1999
ACCESSIONS S52650; S75843
REFERENCE S52649
#authors Sakamoto, T.; Ios, D.A.; Higaashi, S.; Wada, H.; Nishida, I.;
Ohmori, M.; Murata, N.
#journal Plant Mol. Biol. (1994) 26:249-263
#title Cloning of omega-3 desaturase from cyanobacteria and its use
in altering the degree of membrane-lipid unsaturation.
#cross-references M01D:95035996
#accession S52650
#molecule_type DNA
#residues 1-359 ##label SAK
#cross-references GB:D13780; NID:g600596; PID:d1003430; PID:g600598
##note The authors translated the initiation codon GTG for
residue 1 as Val
REFERENCE S74322
#authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hikosawa, M.; Sugita, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Murai, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shingo,
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.
#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular
cyanobacterium Synecocystis sp. PCC6803. II. Sequence
determination of the entire genome and assignment of

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#cross-references MUID:97061201          potential protein-coding regions
#accession      S75843
##status        nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues      1-359 ##label KAN
##cross-references EMBL:D90913; GB:AB001339; NID:g1653348; PID:d1019035
                        PDB:g1653388
##note           the nucleotide sequence was submitted to the EXBL Data
                        Library, June 1996

GENETICS
#start_codon     GTG
CLASSIFICATION    #superfamily omega-3 fatty acid desaturase
KEYWORDS          oxidoreductase
SUMMARY           #length 359 #molecular-weight 41919 #checksum 9162

Query Match      4.0%; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 3,77e-21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPHGMWIRISHRTH 129
   |||||
OY 146 ILVPHGMWIRISHRTH 161

RESULT 13
ENTRY H71349 #type complete
TITLE Probable ribosomal protein L1 (rplA) - syphilis spirochete
ORGANISM #formal_name Treponema pallidum subsp. pallidum #common_name
         syphilis spirochete
DATE 24-Jul-1998 #sequence_revlsion 24-Jul-1998 #ext_change
         17-Mar-1999

ACCESSIONS H71349
REFERENCE A71250
AUTHORS Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.;
         Sutton, G.G.; Dodson, R.; Gwin, M.; Hickey, E.K.; Clayton
         R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod,
         M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson,
         D.; Howell, J.K.; Chidambaram, M.; Uteback, T.; McDonald,
         L.; Artlich, P.; Bowman, C.; Cotton, M.D.; Fujii, C.;
         Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Wetthey,
         L.; Weidman, J.; Smith, H.O.; Venter, J.C.
         Science (1998) 281:375-388
         Complete genome sequence of Treponema pallidum, the syphilis
         spirochete.
#journal #title
#cross-references MUID:98332770
#accession H71349
#status preliminary: nucleic acid sequence not shown;
         translation not shown

##molecule_type DNA
##residues 1-226 ##label COL
##cross-references GB:AEO01205; GB:AEO00520; NID:g3322501; PID:g3322508
##experimental_source strain Nichols

GENETICS
#gene TP0238
CLASSIFICATION #superfamily Escherichia coli ribosomal protein L1
SUMMARY #length 226 #molecular-weight 24977 #checksum 6350

Query Match      2.0%; Score 8; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 5.98e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 83 ALAGAAAY 90
   |||||
OY 88 ALAGAAAY 95

RESULT 14
ENTRY S65770 #type complete
TITLE maltooligosyltrehalose trehalohydrolase - Arthrobaacter sp.
         (strain Q36)
ORGANISM #formal_name Arthrobaacter sp.
         variety strain Q36
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DATE                28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
                        18-Sep-1998
ACCESSIONS          S65770
REFERENCE            S65769
#authors            Maruta, K.; Hattori, K.; Nakada, T.; Kubota, M.; Sugimoto,
                        T.; Kurimoto, M.
#journal             Blochim. Biophys. Acta (1996) 1289:10-13
#title               Cloning and sequencing of trehalose biosynthesis genes from
                        Arthrobacter sp. Q36.
#cross-references    NCID:96195835
#accession           S65770
#status              preliminary
#molecule_type      DNA
#residues             1-538 ##label MAR
#cross-references     EMBL:D65343; NID:g1255444; PID:d1010313; PID:g1255446
CLASSIFICATION       #superfamily_trehalose_trehalohydrolase
SUMMARY              #length 598 #molecular-weight 65831 #checksum 4532

Query Match          2.0%; Score 8; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 5,98e-02;
Matches              8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D6                   8 EAAKPVLG 15
QY                   343 EAAKPVLG 350

RESULT              15
ENTRY               S63399 #type complete
TITLE               probable membrane protein YNR067c - Yeast (Saccharomyces
                        cerevisiae)
ALTERNATE_NAMES      hypothetical protein N3547
ORGANISM             #formal_name Saccharomyces cerevisiae
DATE                 27-Apr-1996 #sequence_revision 03-May-1996 #text_change
                        14-Nov-1997
ACCESSIONS          S63399
REFERENCE            S63944
#authors            Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.;
                        Hilbert, R.; Moestl, D.
#submission          submitted to the Protein Sequence Database, April 1996
#accession           S63399
#molecule_type      DNA
#residues             1-1117 ##label DUE
#cross-references     EMBL:Z71682; NID:g1302597; PID:e239600; PID:g1302598;
                        MIPS:YNR067C
#experimental_source strain S288C

GENETICS
#map_position         14R
KEYWORDS             transmembrane protein
FEATURE              6-22
SUMMARY              #domain transmembrane #status predicted #label TMN
                        #length 1117 #molecular-weight 121063 #checksum 7513

Query Match          2.0%; Score 8; DB 2; Length 1117;
Best Local Similarity 100.0%; Pred. No. 5,98e-02;
Matches              8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D6                   339 TVDSSSP 346
QY                   28 TVDSSSP 35

Search completed: Sat Aug 21 12:32:25 1999
Job time : 60 secs.

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Search completed: Sat Aug 21 12:32:25 1999
Job time : 60 secs.

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 WISE (TM)

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Mpsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:32:42 1999; Maspar time 11.63 Seconds

Tabular output not generated. 981,738 Million cell updates/sec

Title: >US-09-219-935-9
 Description: (1-404) from US09219935.pep
 Perfect Score: 404
 Sequence: 1 FKFROSPSPFRFLNSRNMA.....DYYVYRADNPNGEIKVTAE 404

Scoring table: TABLE unltprotatable
 Gap 60

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 3.728; Variance 0.433; scale 8.613

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score distribution.
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	404	100.0	404	1	FD3C_BRANA OMEGA-3 FATTY ACID DES	0.00e+00
2	103	25.5	446	1	FD3C_ARATH OMEGA-3 FATTY ACID DES	0.00e+00
3	42	10.6	435	1	FD3D_ARATH TEMPERATURE-SENSITIVE	8.21e-111
4	42	10.4	460	1	FD3C_RICCO OMEGA-3 FATTY ACID DES	2.18e-107
5	36	8.9	447	1	FD3C_SESIN OMEGA-3 FATTY ACID DES	5.08e-87
6	36	8.9	453	1	FD3C_SOYBN OMEGA-3 FATTY ACID DES	5.08e-87
7	28	6.9	377	1	FD3I_BRANA OMEGA-3 FATTY ACID DES	1.77e-60
8	28	6.9	383	1	FD3I_BRANA OMEGA-3 FATTY ACID DES	1.77e-60
9	28	6.9	386	1	FD3E_ARATH OMEGA-3 FATTY ACID DES	1.77e-60
10	27	6.2	380	1	FD3E_SOYBN OMEGA-3 FATTY ACID DES	8.86e-51
11	25	6.2	379	1	FD3E_PHAUV OMEGA-3 FATTY ACID DES	8.86e-51
12	24	5.9	379	1	FD3E_TREBA OMEGA-3 FATTY ACID DES	1.38e-47
13	8	2.0	226	1	YNS6_YEAST HYPOTHETICAL 121.1 KD	2.13e-02
14	8	2.0	1117	1	YNS6_YEAST HYPOTHETICAL 121.1 KD	2.13e-02
15	7	1.7	85	1	RLT7_STRGR 50S RIBOSOMAL PROTEIN	2.06e+00
16	7	1.7	100	1	CH10_THETH 10 KD CHAPERONIN (PROT	2.06e+00
17	7	1.7	112	1	AGN5_APLCA ABDOMINAL GANGLION NEU	2.06e+00
18	7	1.7	143	1	SVL_TORCA SYNDOLEIN	2.06e+00
19	7	1.7	213	1	LEAL_HORVU ABA-INDUCIBLE PROTEIN	2.06e+00
20	7	1.7	232	1	Y08E_MYCTU HYPOTHETICAL 23.9 KD P	2.06e+00
21	7	1.7	236	1	LYSE_CORGL LYSINE EXPORTER PROTEIN	2.06e+00
22	7	1.7	280	1	DUS7_RAT DUAL SPECIFICITY PROTE	2.06e+00
23	7	1.7	322	1	DUS7_HUMAN DUAL SPECIFICITY PROTE	2.06e+00

ALIGNMENTS

RESULT	1	STANDARD	PRT	404 AA.
ID	FD3C_BRANA			
AC	P46618;			
DT	01-FEB-1996 (REL. 33, CREATED)			
DT	01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)			
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)			
DE	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-)			
GN	FAO7.			
OS	BRASSICA NAPUS (RAPE).			
OC	EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTES; EMBRYOPHYTES; TRACHEOPHYTES;			
OC	EUPHYLLIPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTES; EUDICOTYLEDONS; ROSIDAE;			
OC	CAPRARIACEAE; BRASSICACEAE; BRASSICA.			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-SEED:			
RX	MEDLINE: 94302147.			
RA	YANAV N.S., WIERZBICKI A., ABERGERT M., CASTER C.S., PEREZ-GRU L.,			
RA	KINNEY A.J., HITE W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,			
RA	ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,			
RT	FELDMANN K.A., PIERCE J., BROWSE J.;			
RL	"Cloning of higher plant omega-3 fatty acid desaturases.";			
CC	PLANT PHYSIOL. 103:467-476(1993).			
CC	-1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES			
CC	THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY			
CC	ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT			
CC	TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS			
CC	ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.			
CC	-1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.			
CC	-1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLY).			
CC	-1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTRAIN THE ACTIVE SITE			
CC	AND/OR BE INVOLVED IN METAL ION BINDING.			
CC	-1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: L22963; G408490; ALT_INIT.			
DR	PIR: P00812; P00812.			
DR	PIR: P00812; P00812.			
DR	PFAM: PF00487; FA_desaturase; 1.			
KW	Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;			
KW	TRANSIT PEPTIDE.			

```

FT  NON_TER 1 1
FT  TRANSIT <1 ?
FT  CHAIN ? 404
FT  DOMAIN 121 125
FT  DOMAIN 157 161
FT  DOMAIN 324 328
SO  SEQUENCE 404 AA: 46617 MW: 79719FB CRC32;

Query Match 100.0%; Score 404; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EFKRSPSSPRRLNSRMALVNTPLVDDSSPPREEPTQRPDGPAPPFNLADIR 60
    1 FFKRSPSSPRRLNSRMALVNTPLVDDSSPPREEPTQRPDGPAPPFNLADIR 60
OY 1 FFKRSPSSPRRLNSRMALVNTPLVDDSSPPREEPTQRPDGPAPPFNLADIR 60
Db 61 AAIPIHCWKNPKMSYVRELATVFAAAGATLNNMLVPLVIAOGTFMALFVLG 120
    61 AAIPIHCWKNPKMSYVRELATVFAAAGATLNNMLVPLVIAOGTFMALFVLG 120
OY 61 AAIPIHCWKNPKMSYVRELATVFAAAGATLNNMLVPLVIAOGTFMALFVLG 120
Db 121 HDGCGSFENDRLNSVYGLHSSILVPGHGRISHTPHONGHVENDESMHPSEKI 180
    121 HDGCGSFENDRLNSVYGLHSSILVPGHGRISHTPHONGHVENDESMHPSEKI 180
OY 121 HDGCGSFENDRLNSVYGLHSSILVPGHGRISHTPHONGHVENDESMHPSEKI 180
Db 181 YKSLDKPTREFFRFTLPVLAIPYTLWARSPPKSGSHVPSDLELPKERNDVLTSTACW 240
    181 YKSLDKPTREFFRFTLPVLAIPYTLWARSPPKSGSHVPSDLELPKERNDVLTSTACW 240
OY 181 YKSLDKPTREFFRFTLPVLAIPYTLWARSPPKSGSHVPSDLELPKERNDVLTSTACW 240
Db 241 TMAVLLVCLNFMVGMOMLKLVIPIYVNVMMVLDVYTLHHGHEDKLPWYRGKEMSTL 300
    241 TMAVLLVCLNFMVGMOMLKLVIPIYVNVMMVLDVYTLHHGHEDKLPWYRGKEMSTL 300
OY 241 TMAVLLVCLNFMVGMOMLKLVIPIYVNVMMVLDVYTLHHGHEDKLPWYRGKEMSTL 300
Db 301 RGLTTLDDYGLINNHHIDISTHVIHHLFPOIPHYLVEATEAKPVLYGKYRREPKSG 360
    301 RGLTTLDDYGLINNHHIDISTHVIHHLFPOIPHYLVEATEAKPVLYGKYRREPKSG 360
OY 301 RGLTTLDDYGLINNHHIDISTHVIHHLFPOIPHYLVEATEAKPVLYGKYRREPKSG 360
Db 361 PPLHLGLILAKSIKEDHFVDEGDVYVYEADPNLYGEIKVTAE 404
    361 PPLHLGLILAKSIKEDHFVDEGDVYVYEADPNLYGEIKVTAE 404
OY 361 PPLHLGLILAKSIKEDHFVDEGDVYVYEADPNLYGEIKVTAE 404

RESULT 2
ID FD3C_ARATH STANDARD; PRT: 446 AA.
AC P46310;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD3 OR FAD3.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC CHLOROPLAST.
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC CAPPARLES: BRASSICACEAE: ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA: TISSUE-HYPOCOTYL.
RX MEDLINE: 94302147.
RA YADAV N.S., WIERBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.O., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA: TISSUE-AERIAL PARTS:
RX MEDLINE: 94043239.
RA IBA K., GIBSON S., NISHUCHI T., FUSE T., NISHIMURA M., ARONDEL V.,
RA HUGLY S., SOMERVILLE C.R.;
RT "A gene encoding a chloroplast omega-3 fatty acid desaturase
complements alterations in fatty acid desaturation and chloroplast

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RT copy number of the fad7 mutant of Arabidopsis thaliana.";
RL J. BIOL. CHEM. 268:24099-24105(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA: TISSUE-HYPOCOTYL.
RA WATANIKI M., YAMAMOTO K.;
RL SUBMITTED (NOV-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GLYCEROLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L22961; G408481; -
DR EMBL: D14007; G541653; -
DR EMBL: D26019; G468434; -
DR PFAM: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW TRANSIT PEPTIDE.
FT TRANSIT 1 ?
FT CHAIN ? 446
FT DOMAIN 163 167
FT DOMAIN 199 203
FT DOMAIN 366 370
SO SEQUENCE 446 AA: 51174 MW: 8DE08779 CRC32;

Query Match 25.5%; Score 103; DB 1; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPYWINVWMLDFVYTLHHGHEDKLPWYRGKEMSTLRGLTTLDDYGLINNHHIDISTH 366
    307 IPYWINVWMLDFVYTLHHGHEDKLPWYRGKEMSTLRGLTTLDDYGLINNHHIDISTH 366
OY 265 IPYWINVWMLDFVYTLHHGHEDKLPWYRGKEMSTLRGLTTLDDYGLINNHHIDISTH 324
Db 367 VIHHLFPOIPHYLVEATEAKPVLYGKYRREPKSGPPLHLL 409
    367 VIHHLFPOIPHYLVEATEAKPVLYGKYRREPKSGPPLHLL 409
OY 325 VIHHLFPOIPHYLVEATEAKPVLYGKYRREPKSGPPLHLL 367

RESULT 3
ID FD3D_ARATH STANDARD; PRT: 435 AA.
AC P48622;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
DE PRECURSOR (EC 1.14.99.-).
GN FAD8.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC CAPPARLES: BRASSICACEAE: ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA: TISSUE-AERIAL PARTS:
RX MEDLINE: 95148742.
RA GIBSON S., ARONDEL V., IBA K., SOMERVILLE C.R.;
RT "Cloning of a temperature-regulated gene encoding a chloroplast

```

RT Omega-3 desaturase from Arabidopsis thaliana.";
RL PLANT PHYSIOL. 106:1615-1621(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA: TISSUE-HYPOCOTYL;
RA WATANAKI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L27158; G516045; -
DR EMBL: U08216; G497219; -
DR EMBL: D17578; G471093; -
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT TRANSIT 1 ?
FT CHAIN 1 435 CHLOROPLAST (POTENTIAL).
FT FT 1 435 TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID
FT DOMAIN 156 160 HISTIDINE BOX 1.
FT DOMAIN 192 196 HISTIDINE BOX 2.
FT DOMAIN 359 363 HISTIDINE BOX 3.
SQ SEQUENCE 435 AA; 50136 MW; 70613FE0 CRC32;
Query Match 10.6%; Score 43; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 8,21e-111;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 349 INNHHIDGTHVHHLPQIPHVLVEATEAKPVLGKTYREP 391
Y 314 INNHHIDGTHVHHLPQIPHVLVEATEAKPVLGKTYREP 356
RESULT 4
ID FD3C.RICCO STANDARD; PRT; 460 AA.
AC P48619;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7A-1.
OS RICINUS COMMUNIS (CASTOR BEAN).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMERIOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC EUPHORBIALES; EUPHORBIACEAE; RICINUS.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. BAKER 296; TISSUE-SEED;
RA MEDLINE; 9430217.
RA VAN DE LOO F.J., SOMERVILLE C.R.;
RT "Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.";
RL PLANT PHYSIOL. 105:443-444(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL: U25817; G870784; -
DR PFAM: PF00487; FA_desaturase; 1.

CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L25897; G414732; -
DR PFAM: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT TRANSIT 1 ?
FT CHAIN 1 460 CHLOROPLAST (POTENTIAL).
FT FT 1 460 OMEGA-3 FATTY ACID DESATURASE,
FT DOMAIN 177 181 HISTIDINE BOX 1.
FT DOMAIN 213 217 HISTIDINE BOX 2.
FT DOMAIN 380 384 HISTIDINE BOX 3.
SQ SEQUENCE 460 AA; 52561 MW; DB3DA689 CRC32;
Query Match 10.4%; Score 42; DB 1; Length 460;
Best Local Similarity 100.0%; Pred. No. 2,18e-107;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 190 LNSVGHLSHSILVPGHGRISHRTGHNGHVENDESWP 231
Y 134 LNSVGHLSHSILVPGHGRISHRTGHNGHVENDESWP 175
RESULT 5
ID FD3C.SESIN STANDARD; PRT; 447 AA.
AC P48620;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7.
OS SESAMUM INDICUM (ORIENTAL SESAME) (GINNELLY).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMERIOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANANAE; LAMIALES; PEDALACEAE; SESAMUM.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. 4294; TISSUE-COTYLEDON;
RA SHOUT K.;
RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U25817; G870784; -
DR PFAM: PF00487; FA_desaturase; 1.

KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 KM TRANSIT PEPTIDE.
 FT TRANSIT 1. CHLOROPLAST (POTENTIAL).
 FT CHAIN ? 447 OMEGA-3 FATTY ACID DESATURASE,
 CHLOROPLAST.
 FT DOMAIN 167 171 HISTIDINE BOX 1.
 FT DOMAIN 203 207 HISTIDINE BOX 2.
 FT DOMAIN 370 374 HISTIDINE BOX 3.
 SQ SEQUENCE 447 AA; 51116 MW; 67B2C46B CRC32;

Query Match 8.9%; Score 36; DB 1; Length 447;
 Best Local Similarity 100.0%; Pred. No. 5.08e-87;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D0 323 VTYLHHGHEDKLPWYRGKESYLRGGLTLLDRYG 358
 ||||||||||||||||||||||||||||||||||||
 OY 277 VTYLHHGHEDKLPWYRGKESYLRGGLTLLDRYG 312

RESULT 6
 ID FD3C_S0YBN STANDARD; PRT; 453 AA.
 AC P46821;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
 GN FAD7.
 OS EUCARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 CC CAPRARIACE; BRASSICACEAE; PAPILIONOIDEAE; GLYCINE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SEED;
 RX MEDLINE; 94302147.
 RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAT L.,
 KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
 ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 FELDMAN K.A., PIERCE J., BROWSE J.;
 RA "Cloning of higher plant omega-3 fatty acid desaturases.";
 RT PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 AND 18:3 FATTY
 ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTRAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.

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 CC -----
 CC EMBL; L22965; G408792; -.
 DR PIR; JQ2339; JQ2339.
 DR PIR; JQ2339; JQ2339.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 KM TRANSIT PEPTIDE.
 FT TRANSIT 1. CHLOROPLAST (POTENTIAL).
 FT CHAIN ? 453 OMEGA-3 FATTY ACID DESATURASE,
 CHLOROPLAST.
 FT DOMAIN 171 175 HISTIDINE BOX 1.
 FT DOMAIN 207 211 HISTIDINE BOX 2.
 FT DOMAIN 374 378 HISTIDINE BOX 3.
 SQ SEQUENCE 453 AA; 51362 MW; E4314F1B CRC32;

Query Match 8.9%; Score 36; DB 1; Length 453;
 Best Local Similarity 100.0%; Pred. No. 5.08e-87;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D0 327 VTYLHHGHEDKLPWYRGKESYLRGGLTLLDRYG 362
 ||||||||||||||||||||||||||||||||||||
 OY 277 VTYLHHGHEDKLPWYRGKESYLRGGLTLLDRYG 312

RESULT 7
 ID FD3L_BRANA STANDARD; PRT; 377 AA.
 AC P46311;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
 GN FAD3.
 OS BRASSICA NAPUS (RAPE).
 OC EUCARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 CC CAPRARIACE; BRASSICACEAE; BRASSICA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SEED;
 RX MEDLINE; 94302147.
 RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAT L.,
 KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
 ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 FELDMAN K.A., PIERCE J., BROWSE J.;
 RA "Cloning of higher plant omega-3 fatty acid desaturases.";
 RT PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTRAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.

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 CC -----
 CC EMBL; L22962; G408492; -.
 DR PIR; JQ2339; JQ2339.
 DR PIR; JQ2339; JQ2339.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KM TRANSMEMBRANE.
 FT TRANSMEM 54 73 POTENTIAL.
 FT TRANSMEM 203 226 POTENTIAL.
 FT TRANSMEM 233 251 POTENTIAL.
 FT DOMAIN 92 96 HISTIDINE BOX 1.
 FT DOMAIN 128 132 HISTIDINE BOX 2.
 FT DOMAIN 295 299 HISTIDINE BOX 3.
 SQ SEQUENCE 377 AA; 43258 MW; 247237E0 CRC32;

Query Match 6.9%; Score 28; DB 1; Length 377;
 Best Local Similarity 100.0%; Pred. No. 1.77e-60;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D0 117 ILVYHGWRISHRTTHONHGVENDESM 144
 ||||||||||||||||||||||||||||||||
 OY 146 ILVYHGWRISHRTTHONHGVENDESM 173

RESULT 8
ID F032_BRNA STANDARD: PRT: 383 AA.
AC P48624;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (VERSION 2).
GN FAD3.
OS BRASSICA NAPUS (RAPE).
OC EUCHAROTA: VIRIDIPHYTES: STREPTOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES:
OC EUCHAROTA: VIRIDIPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS: ROSIDAE:
OC CAPRALES: BRASSICACEAE: BRASSICA.
RN
RP
RX MEDLINE: 93088059.
RA ARONDEL V., LEMIEUX B., HWANG I., GIBSON S., GOODMAN H.M.,
RA SOMERVILLE C.R.;
RT "Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis.";
RL SCIENCE 258:1353-1355(1992).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL: L01418; G167148; -
DR PFM: PF00487; FA:desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 210 230 POTENTIAL.
FT TRANSMEM 234 254 POTENTIAL.
FT DOMAIN 98 102 HISTIDINE BOX 1.
FT DOMAIN 134 138 HISTIDINE BOX 2.
FT DOMAIN 301 305 HISTIDINE BOX 3.
SQ SEQUENCE 383 AA; 43936 MW; F39A978B CRC32;
Query Match 6.9%; Score 28; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.77e-60;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 123 ILVPHGWRISHRTHQNHGVNDESW 150
QY 146 ILVPHGWRISHRTHQNHGVNDESW 173

OC CAPRALES: BRASSICACEAE; ARABIDOPSIS.
RN
RP
RX MEDLINE: 94302147.
RA YADAV N.S., WIERZBICT A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITE W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMANN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
RN
RP
RX MEDLINE: 94345020.
RA NISHIOCHI T., NISHIMURA M., ARONDEL V., IBA K.;
RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
RT fatty acid desaturase from Arabidopsis thaliana.";
RL PLANT PHYSIOL. 105:767-768(1994).
RN
RP
RX MEDLINE: 94345020.
RA SIKES S.M., NAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
RA SOMERVILLE C.R., VENTER J.C.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: MICROSMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
CC DETECTABLE IN ROOT TISSUE.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL: L22931; G408483; -
DR EMBL: D17579; G471091; -
DR EMBL: D26508; G119795; -
DR EMBL: AC004680; G3420053; -
DR PFM: PF00487; FA:desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 220 240 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
FT DOMAIN 101 105 HISTIDINE BOX 1.
FT DOMAIN 137 141 HISTIDINE BOX 2.
FT DOMAIN 304 308 HISTIDINE BOX 3.
SQ SEQUENCE 386 AA; 44076 MW; C22B4B8C CRC32;
Query Match 6.9%; Score 28; DB 1; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.77e-60;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 126 ILVPHGWRISHRTHQNHGVNDESW 153

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Oy 146 ILVPHGWRISRTHRHQNGHVENDESW 173
|||||
RESULT 10
ID FD3E_S0YBN STANDARD: PRT: 380 AA.
AC P48625;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
GN FAD3.
OS GLUCINE MAX (SOYBEAN).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RX MEDLINE: 94302147.
RA YADAV N.S., WIERZICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ M.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.;
RT Cloning of higher plant omega-3 fatty acid desaturases."
RL PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: MICROSOML (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
DR EMBL: J22964; G408794; -.
DR PIR: JQ2338; JQ2338.
DR PFAM: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 100 104 HISTIDINE BOX 1.
FT DOMAIN 136 140 HISTIDINE BOX 2.
FT DOMAIN 303 307 HISTIDINE BOX 3.
FT SEQUENCE 380 AA; 44185 MW; E3C509B7 CRC32;
SQ
Query Match 6.7%; Score 27; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.17e-57;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).
GN ARG1.
OS PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC FABALES; FABACEAE; PAPILIONOIDEAE; VIGNA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOCOTYL;
RX YANAMOTO K.T., MORI H., IMASEKI H.;
RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
RT elongating hypocotyls of mung bean (Vigna radiata).";
RL PLANT CELL PHYSIOL. 33:13-20(1992).
CC -1- FUNCTION: MICROSOML (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D14410; G287562; -.
DR PFAM: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 59 78 POTENTIAL.
FT TRANSMEM 208 231 POTENTIAL.
FT TRANSMEM 238 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
FT SEQUENCE 380 AA; 43996 MW; 8429BF68 CRC32;
SQ
Query Match 6.2%; Score 25; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 8.86e-51;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Length
Query Match	8	2.0%	Score 8	DB 1	Length 1117	
Matches	8	Conservative	0	Mismatches	0	Indels
						Gaps
						0

Db 339 TVDSSSSP 346
 |||||
 Oy 28 TVDSSSSP 35

RESULT 15
 ID RI27_STRGR STANDARD: PRT: 85 AA.

AC P95737;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE 505 RIBOSOMAL PROTEIN L27.
 GN RPLA.
 OS STREPTOMYCES GRISEUS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-IFO 13189;
 RX MEDLINE; 97136618.
 RA OKAMOTO S., ITOH M., OCHI K.;
 RT "Molecular cloning and characterization of the obp gene of
 RT Streptomyces griseus in relation to the onset of morphological
 RT differentiation."
 RL J. BACTERIOL. 179:170-179(1997).
 CC -!- SIMILARITY: BELONGS TO THE L27P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----

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 CC -----

DR EMBL: D87916; G1783293; -.
 DR PROSITE: PS00831; RIBOSOMAL_L27; 1.
 DR PFM: PFO1016; Ribosomal_L27; 1.
 KW RIBOSOMAL PROTEIN.
 SQ SEQUENCE 85 AA; 8860 MW; 804E9523 CRC32;

Query Match 1.7%; Score 7; DB 1; Length 85;
 Best Local Similarity 100.0%; Pred. No. 2.06e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 FALAAGA 66
 |||||
 Oy 87 FALAAGA 93

Search completed: Sat Aug 21 12:33:03 1999
 Job time : 21 secs.

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:33:21 1999; MasPar time 23.83 Seconds

Tabular output not generated. 925.332 Million cell updates/sec

Title: >US-09-219-935-9

Description: (1-404) from US09219935.pep

Sequence: 1 FKFQSPSSPFRFLNSRNMA.....DVYYEADPNLXGEIKVTAE 404

Scoring table: TABLE uniprotatable

Gap 60

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: sptrembl9

1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus

Statistics: Mean 3.632; Variance 0.453; scale 8.025

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	47	11.6	436 10	Q40118	DELTA-15 LINEOYL DESAT	2.00e-116
2	43	10.6	398 10	Q24626	FATTY ACID DESATURASE	1.44e-103
3	40	9.9	431 10	082068	W-3 DESATURASE	5.41e-94
4	40	9.9	441 10	P93350	OMEGA-3 FATTY ACID DES	5.41e-94
5	37	9.2	438 10	004807	OMEGA-3 FATTY ACID DES	1.74e-81
6	36	8.9	443 10	023824	FATTY ACID DESATURASE	2.46e-81
7	34	8.4	438 10	P93452	OMEGA-3 FATTY ACID DES	4.63e-75
8	29	7.2	381 10	P94013	W-3 FATTY ACID DESATUR	1.43e-59
9	29	7.2	383 10	065792	OMEGA-3 FATTY ACID DES	1.43e-59
10	28	6.9	407 10	064907	OMEGA-3 DESATURASE (FR	1.64e-56
11	24	5.9	380 10	023802	PLASTID OMEGA-3 FATTY	1.32e-44
12	16	4.0	359 2	035240	DELTA-15 DESATURASE	1.76e-21
13	11	2.7	350 2	007872	FATTY ACID DESATURASE	1.41e-08
14	8	2.0	193 3	074645	FATTY ACID DESATURASE	6.19e-02
15	8	2.0	598 2	044316	MALTOLOIGOSYL TREHALOS	6.19e-02
16	8	2.0	4848 2	007944	PRISTINAMYCIN I SYNTHA	6.19e-02
17	7	1.7	92 10	P93687	REVERSE TRANSCRIPTASE	4.91e+00
18	7	1.7	138 5	023434	K1251.7 PROTEIN	4.91e+00
19	7	1.7	224 10	003968	LATE EMBRYOGENESIS ABU	4.91e+00
20	7	1.7	284 2	Q54080	ORF1.	4.91e+00

RESULT	ID	PRELIMINARY	PRT	436 AA.	ALIGNMENTS
AC	Q40118				
DT	01-NOV-1996 (TREMBL,REL. 01, CREATED)				
DT	01-NOV-1996 (TREMBL,REL. 01, LAST SEQUENCE UPDATE)				
DT	01-JAN-1999 (TREMBL,REL. 09, LAST ANNOTATION UPDATE)				
DE	DELTA-15 LINEOYL DESATURASE.				
OS	LIMNANTHES DOUGLASSII.				
OC	EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:				
OC	EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:				
OC	CAPPALES: LIMNANTHACEAE: LIMNANTHES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 95334518.				
RA	BHELIA R.S., MACKENZIE S.L.:				
RT	"Nucleotide sequence of a cDNA from Limnantes douglasii L. encoding				
RT	a delta-15 linoleic acid desaturase."				
RL	PLANT PHYSIOL. 108:861-861(1995).				
DR	EMBL: U17063; G699390; -.				
DR	PFAM: PF00487; FA desaturase; 1.				
DR	MENDEL: 8699; Limdo:1208:1.				
SO	SEQUENCE 436 AA; 50093 MW; 327D77FE CRC32;				

Query Match 11.6%; Score 47; DB 10; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.00e-116;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT	ID	PRELIMINARY	PRT	398 AA.
AC	Q24626			
DT	01-JAN-1998 (TREMBL,REL. 05, CREATED)			
DT	01-JAN-1998 (TREMBL,REL. 05, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBL,REL. 08, LAST ANNOTATION UPDATE)			
DE	FATTY ACID DESATURASE (FRAGMENT).			
GN	FAD8.			
OS	ZEA MAYS (MAIZE).			
OC	EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:			
OC	EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: LILIOPSIDA: POALES;			
OC	POACEAE; ZEA.			

Db 330 EWSIRGGLTLDYDYGILNNIHHDIGTHVTHHPQIPHYHLYEAT 376
QY 296 EWSYLRGGLTLDYDYGILNNIHHDIGTHVTHHPQIPHYHLYEAT 342

[1]
RN SEQUENCE FROM N.A.
RC STRAIN-HONEY BANTAM AND HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
DR EMBL: D84409; D1023307; -;
DR EMBL: D63953; D1023305; -;
DR PRAW; PF00487; FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 398 AA; 44789 MW; 70565SEC CRC32;

Query Match 10.6%; Score 43; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 1,44e-103;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 EMSYLRGGLTLDRLDYLINNIHHDIGTHVHHLFPOIPHYHL 333
OY 296 EMSYLRGGLTLDRLDYLINNIHHDIGTHVHHLFPOIPHYHL 338
|||||

RESULT 3
ID 082068; PRELIMINARY; PRT; 431 AA.
AC 082068;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE W-3 DESATURASE.
OS SOLANUM TUBEROSUM (POTATO).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
CC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
CC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; SOLANUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RA LEON J.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RA MARTIN M.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ007739; E1318202; -;
SQ SEQUENCE 431 AA; 49253 MW; BAFAP9CD CRC32;

Query Match 9.9%; Score 40; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 5,41e-94;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 345 INNIHHDIGTHVHHLFPOIPHYHLVEATEAKPVLGKRY 384
OY 314 INNIHHDIGTHVHHLFPOIPHYHLVEATEAKPVLGKRY 353
|||||

RESULT 4
ID P93350; PRELIMINARY; PRT; 441 AA.
AC P93350;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
GN NTERAD7
OS NICOTIANA TABACUM (COMMON TOBACCO).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
CC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
CC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; NICOTIANA.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 96416425.
RA HANADA T., NISHIGUCHI T., KODAMA H., NISHIMURA M., IBA K.;
RT "cDNA cloning of a wounding-inducible gene encoding a plastid omega-3
fatty acid desaturase from tobacco."
RL PLANT CELL PHYSIOL. 37:606-611(1996).
DR EMBL: D79979; D1012141; -;

DR PRAW; PF00487; FA_desaturase; 1.
DR MENDEL; 9312; Nicta;1208;2.
SQ SEQUENCE 441 AA; 50310 MW; 255F96A6 CRC32;

Query Match 9.9%; Score 40; DB 10; Length 441;
Best Local Similarity 100.0%; Pred. No. 5,41e-94;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 355 INNIHHDIGTHVHHLFPOIPHYHLVEATEAKPVLGKRY 394
OY 314 INNIHHDIGTHVHHLFPOIPHYHLVEATEAKPVLGKRY 353
|||||

RESULT 5
ID 004807; PRELIMINARY; PRT; 438 AA.
AC 004807;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PERILLA FRUTESCENS.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
CC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
CC ASTERIDAE; GENTIANACEAE; LAMIALES; LAMIACEAE; PERILLA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OKDONG;
RA LEE S.K., KIM K.H., KIM Y.M., HWANG Y.S.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U55477; G1754795; -;
DR PRAW; PF00487; FA_desaturase; 1.
DR MENDEL; 16268; PERIT;1208;ml6268.
SQ SEQUENCE 438 AA; 50160 MW; EE726819 CRC32;

Query Match 9.2%; Score 37; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 1,74e-84;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 GHLHSSILVYHGMWRISRTRHONHGHVDESWHP 217
OY 139 GHLHSSILVYHGMWRISRTRHONHGHVDESWHP 175
|||||

RESULT 6
ID 023824; PRELIMINARY; PRT; 443 AA.
AC 023824;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE.
GN FAD7
OS ZEA MAYS (MAIZE).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
CC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
CC POACEAE; ZEA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
RN [2]
RP SEQUENCE OF 182-443 FROM N.A.
RC STRAIN-HONEY BANTUM;
RX MEDLINE; 98145435.
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RT "Two maize genes encoding omega-3 fatty acid desaturase and their
differential expression to temperature."
RL PLANT MOL. BIOL. 36:297-306(1998).
DR EMBL: D63954; D1023306; -;
DR EMBL: D63952; D1023304; -;
DR PRAW; PF00487; FA_desaturase; 1.
SQ SEQUENCE 443 AA; 49637 MW; E8B6757 CRC32;

RESULT 9

RESULT	11		
ID	023802	PRELIMINARY;	PRT; 380 AA.
AC	023802;		
DT	01-JAN-1998 (TREMBL.NL, 05, CREATED)		
DJ	01-JAN-1998 (TREMBL.NL, 05, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998 (TREMBL.NL, 08, LAST ANNOTATION UPDATE)		
DE	PLASTID OMEGA-3 FATTY ACID DESATURASE (FRAGMENT).		
GN	TAFAD7.		
OS	TRITICUM AESTIVUM (WHEAT).		
OC	EUKARYOTA: VIRIDIPLANTEAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA.		
OC	EUPHYLOPHITES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;		
OC	POACEAE; TRITICUM.		
CC	[1]		
RN	SEQUENCE FROM N. A.		
RC	STRAIN-CV. CHIKOKU; TISSUE-LEAF;		
RA	HORIUCHI G., IMAKAWA H., KOYAMA H., KAWAKAMI N., NISHIMURA M.,		

RA IRA K.;
RL PHYSIOL. PLANTARUM 96:275-283(1996).
DR EMBL; D43688; D1008371; -.
DR PFAM; PF00487; FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 380 AA; 42633 MW; 2123FF56 CRC32;
Query Match 5.9%; Score 24; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.92e-44;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 130 GWRISHRTHQNHGVNDESMWP 153
152 GWRISHRTHQNHGVNDESMWP 175
RESULT 12
ID 055240 PRELIMINARY; PRT; 359 AA.
AC 055240;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE DELTA 15 DESATURASE.
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95035996.
RA SAKAMOTO T., LOS D.A., HIGASHI S., WADA H., NISHIDA I., OHMORI M.,
MURATA N.;
RT "Cloning of omega 3 desaturase from cyanobacteria and its use in
altering the degree of membrane-lipid unsaturation.";
RL PLANT MOL. BIOL. 26:249-263(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA TABATA S.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSHIMA M., SUGIURA M., SASAKOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RL DNA RES. 3:109-136(1996).
DR EMBL; D13780; G600598; -.
DR EMBL; D90913; G1653388; -.
DR PFAM; PF00487; FA_desaturase; 1.
SQ SEQUENCE 359 AA; 41919 MW; B5375D98 CRC32;
Query Match 4.0%; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.76e-21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 114 ILVPHGWRISHRTH 129
146 ILVPHGWRISHRTH 161
RESULT 13
ID 007872 PRELIMINARY; PRT; 350 AA.
AC 007872;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE OMEGA-3 DESATURASE.
OS DESB.
OS SYNECHOCOCCUS PCC7002.

OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97260123.
RA SAKAMOTO T., BRYANT D.A.;
RT "Temperature-regulated mRNA accumulation and stabilization for fatty
acid desaturase genes in the cyanobacterium Synechococcus sp. strain
PCC 7002.";
RL MOL. MICROBIOL. 23:1281-1292(1997).
DR EMBL; U36389; G2197199; -.
DR PFAM; PF00487; FA_desaturase; 1.
SQ SEQUENCE 350 AA; 40562 MW; 969CAD61 CRC32;
Query Match 2.7%; Score 11; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.41e-08;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 74 ACGTMEWALFY 84
108 ACGTMEWALFY 118
RESULT 14
ID 074645 PRELIMINARY; PRT; 193 AA.
AC 074645;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
OS GIBBERELLA ZEAE.
OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
OC HYPOCREALES; HYPOCREACEAE; GIBBERELLA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-F15;
RC MEDLINE; 98433864.
RA KIMURA M., MATSUMOTO G., SHINGU Y., YONEYAMA K., YAMAGUCHI I.;
RT "The mystery of the trichothecene 3-O-acetyltransferase gene.
Analysis of the region around trl101 and characterization of its
RT homologue from Fusarium sporotrichioides.";
RL FEBS LETT. 435:163-168(1998).
DR EMBL; AB014492; D1034743; -.
FT NON_TER 1
FT NON_TER 193
SQ SEQUENCE 193 AA; 21845 MW; BF2053ED CRC32;
Query Match 2.0%; Score 8; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.19e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 186 HVHHLFP 193
324 HVHHLFP 331
RESULT 15
ID 044316 PRELIMINARY; PRT; 598 AA.
AC 044316;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE MALTOLOGOSYL TREHALOSE TREHALOHYDROLASE.
GN TREZ.
OS ARTHROBACTER SP.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIAE;
OC ACTINOMYCETES; MICROCOCCINAE; MICROCOCCACEAE; ARTHROBACTER.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-Q36;
RX MEDLINE; 96195835.
RA MARUTA K., HATORI K., NAKADA T., KUBOTA M., SUGIMOTO T., KURIMOTO M.;
RT "Cloning and sequencing of trehalose biosynthesis genes from
Arthrobacter sp. Q36.";

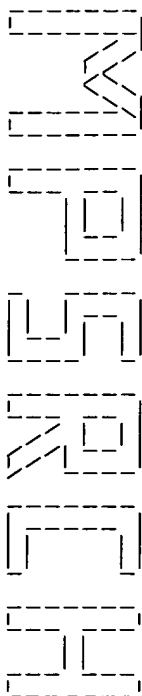
RL BIOCHIM. BIOPHYS. ACTA 1289:10-13(1996).
 DR EMBL; D63343; D1010313; -;
 DR PFAM; PF00128; alpha-amylase; 1.
 KW HYDROLASE.

SQ SEQUENCE 598 AA; 65832 MW; 22719107 CRC32;
 Query Match 2.0%; Score 8; DB 2; Length 598;
 Best Local Similarity 100.0%; Pred. No. 6.19e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 EAKKPVLG 15
 |||||
 OY 343 EAKKPVLG 350

Search completed: Sat Aug 21 12:34:52 1999
 Job time : 91 secs.

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MSPRCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:29:12 1999; MasPar time 15.63 Seconds

Tabular output not generated. 549,751 Million cell updates/sec

Title: MUS-09-219-935-9

Description: (1-404) from US09219935.pep

Perfect Score: 404

Sequence: 1 KFKRQSPSPFRRLNSRWMA.....DVYYEADPNLYGEIKVTAE 404

Scoring table: TABLE uniprottable

Gap 60

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

a:geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 2.916; Variance 0.702; scale 4.153

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	404	100.0	404	7	R37594	Sequence of plastid d	0.00e+00
2	378	93.6	378	7	R37591	Sequence of microsoma	0.00e+00
3	103	25.5	446	11	R60499	Linoic-acid-desatur	9.37e-160
4	103	25.5	446	7	R37593	Sequence of a plastid	9.37e-160
5	43	10.6	435	11	R60500	Linoic-acid-desatur	9.96e-56
6	36	8.9	447	24	W13381	Sesame omega-3 alipha	5.93e-44
7	36	8.9	453	7	R37596	Sequence of soybean p	5.93e-44
8	30	7.4	156	7	R37598	Sequence of a plastid	5.28e-34
9	28	6.9	383	11	R60498	Linoic-acid-desatur	1.00e-30
10	28	6.9	386	7	R37592	Sequence of delta-15	1.00e-30
11	27	6.7	380	7	R37595	Sequence of microsoma	4.27e-29
12	9	2.2	126	7	R37597	Sequence of an intern	7.93e-02
13	9	2.2	387	10	R53700	Sequence of corn micr	7.93e-02
14	8	2.0	20	14	R80284	Trehalose releasing e	1.43e+00
15	8	2.0	597	14	R80290	Trehalose releasing e	1.43e+00
16	8	2.0	598	14	R77471	Trehalose releasing e	1.43e+00

Result	Score	Query Match	Length	DB	ID	Description	Pred. No.
17	7	1.7	18	17	R88585	Spider venom calcium	2.21e+01
18	7	1.7	18	2	R07633	N-terminal of Fractio	2.21e+01
19	7	1.7	18	8	R38424	Aperita venom fracti	2.21e+01
20	7	1.7	236	26	W37715	C. glutamicum lys E p	2.21e+01
21	7	1.7	289	19	W01128	Coat protein (short v	2.21e+01
22	7	1.7	367	19	R98899	Coat protein (long v	2.21e+01
23	7	1.7	367	34	W61492	Human fetuin glycopro	2.21e+01
24	7	1.7	663	4	R24101	Marek's disease virus	2.21e+01
25	6	1.5	202	39	W67822	Human secreted protei	2.77e+02
26	6	1.5	203	39	W67898	Human secreted protei	2.77e+02
27	6	1.5	214	2	R10281	Simian immunodefici	2.77e+02
28	6	1.5	239	36	W80690	S. pneumoniae protein	2.77e+02
29	6	1.5	424	39	W86150	Human growth-related	2.77e+02
30	6	1.5	424	36	W79959	Human growth-related	2.77e+02
31	6	1.5	438	39	W95500	Campylobacter jejuni	2.77e+02
32	6	1.5	493	39	W84068	B. subtilis yade rela	2.77e+02
33	6	1.5	519	39	W89782	Human mitofusin Fzo h	2.77e+02
34	6	1.5	539	22	W17973	Staphylococcus aureus	2.77e+02
35	6	1.5	549	38	W37053	Coprinus cinereus lcc	2.77e+02
36	6	1.5	549	38	W70898	S. putrefaciens EPO b	2.77e+02
37	6	1.5	707	38	W83395	Acetyl-coenzyme A tra	2.77e+02
38	6	1.5	708	38	W83395	Rabbit protein-couple	2.77e+02
39	6	1.5	1012	39	W95395	Human protein-couple	2.77e+02
40	6	1.5	1978	35	W69361	IBDV VP2-VP3-VP4 poly	2.77e+02
41	6	1.5	1988	35	W69362	Tetradotoxin-sensitiv	2.77e+02
42	6	1.5	2100	39	W89579	Retrodotoxin-sensitiv	2.77e+02
43	6	1.5	2104	39	W89579	Calcium permeable vol	2.77e+02
44	6	1.5	2105	39	W89577	Calcium permeable vol	2.77e+02
45	6	1.5	2132	23	W21739	Calcium permeable vol	2.77e+02
						Variant rat DRG (SNS-	2.77e+02

ALIGNMENTS

RESULT 1
ID R37594 standard; Protein: 404 AA.
AC R37594;
DE 01-OCT-1993 (first entry)
KW Sequence of plastid delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus; clone pBNSFd-2.
PN W09311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU POINT DE NEMOURS & CO E. I.
PI Browne J, Gran LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; Q43206.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT acid desaturase or related enzyme with high aminoacid identity to
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide.
PS Disclosure; Page 140-141; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from PCF3 and PCM2 were used to isolate pBNSFd-3. Plasmid pBNSFd-3
CC was deposited as ATCC No. 68854. pBNSFd-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 404 AA:
Query Match 100.0%; Score 404; DB 7; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43204.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 132-134; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q4324. In contrast to the
CC constitutive expression of the gene encoding (R37592), the mRNA
CC corresponding to Q43204 is abundant in green tissues, rare in roots
CC and leaves, and is about three-fold more abundant in leaf than that
CC of Q43202. R37592 and R37593 show and overall homology of approx.
CC 80%.

SO Sequence 446 AA;

Query Match 25.58; Score 103; DB 7; Length 446;
Best Local Similarity 100.0%; Pred. No. 9.37e-160;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 lpywtvwmwldfttylhbhbkelpyrgkewylrglttdrgylnnhhdgth 366
|||||
QY 265 lptwimwldfttylhbhbkelpyrgkewylrglttdrgylnnhhdgth 324
|||||

Db 367 vlhhlfqdlphylveateakpvlqkyrepdkspdlphll 409
|||||
QY 325 vlhhlfqdlphylveateakpvlqkyrepdkspdlphll 367
|||||

RESULT 5
ID R60500 standard; Protein: 435 AA.
AC R60500;
DT 28-MAR-1995 (first entry)
DE linoletic-acid-desaturase fadE.
KW linoletic-acid-desaturase; fadE; transgenic plant; crop improvement;
KM linoletic acid.
OS Arabidopsis.
PN MO9418337-A.
PD 18-AUG-1994.
PE 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PA (UNMS) UNIV MICHIGAN STATE.
PI Aronold VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
DR WPI: 94-279758/34.
DR N-PSDB: Q71211.
PT Genetically transformed plants with altered linoletic acid
PT content - cont recombinant, double-stranded DNA encoding
PT linoletic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure: Page 79-81; 144pp; English.
CC The cDNA sequence and deduced amino acid sequence of linoletic-
CC acid-desaturase fadE of Arabidopsis are provided.
SQ Sequence 435 AA;

Query Match 10.68; Score 43; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 9.96e-56;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 lnnhhdgthvhlhlfqdlphylveateakpvlqkyrep 391
|||||
QY 314 lnnhhdgthvhlhlfqdlphylveateakpvlqkyrep 356
|||||

RESULT 6
ID W13381 standard; Protein: 447 AA.
AC W13381;
DT 02-DEC-1997 (first entry)
DE Sesame omega-3 aliphatic acid desaturase.
KW Sesame; omega-3 aliphatic acid desaturase; modify; fat; oil; plant;
KW linoletic acid; recombinant production.
OS Sesamum indicum.
PN J09065882-A.
PD 11-MAR-1997.
PE 01-SEP-1995; 225145.
PR (TOYA-) TOYAMA KEN.
PA WPI: 97-220417/20.
DR N-PSDB: T62066.
PT Sesame omega-3 aliphatic acid desaturase gene - useful in genetic
PT engineering to modify fats and oils in agricultural products
PS Claim 6; Page 4; 10pp; Japanese.
CC This protein is a sesame omega-3 aliphatic acid desaturase. Its coding
CC sequence can be used in genetic engineering to modify fats and oils in
CC agricultural products. The gene or enzyme can be introduced into a plant
CC to modify the aliphatic acid composition in its oils and fats, to give
CC oils and fats with a high content of linoletic acid. Antisense DNA can
CC be introduced into a plant to inhibit the expression of the gene, so
CC that oils and fats with little or no linoletic acid are produced. The
CC gene can also be expressed in microorganisms for recombinant production
CC the enzyme.

SO Sequence 447 AA;

Query Match 8.98; Score 36; DB 24; Length 447;
Best Local Similarity 100.0%; Pred. No. 5.93e-44;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 323 vtylhbhgdhklpyrgkewylrglttdrgy 358
|||||
QY 277 vtylhbhgdhklpyrgkewylrglttdrgy 312
|||||

RESULT 7
ID R37596 standard; Protein: 453 AA.
AC R37596;
DT 01-OCT-1993 (first entry)
DE Sequence of soybean plastid delta-15 desaturase.
KM Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max. clone pSPD-118bwp.
PN MO9311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43208.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 148-150; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q4324. Arabidopsis delta-15

CC desaturase cDNA was used as a hybridization probe to isolate a
 CC glycerolipid desaturase cDNA from soybean. Plasmid pXf1 was
 CC deposited under ATCC 68874. Soybean microsomal delta-15
 CC desaturase cDNA was used as a hybridization probe to isolate cDNAs
 CC encoding related desaturases from soybean. The insert of
 CC pSFD-118bp contained a stretch of 1675 nucleotides which contained
 CC an open-reading frame encoding a polypeptide (R37596) of about
 CC 80% identity with, and colinear with, the Arabidopsis plastid
 CC delta-15 desaturase polypeptide listed in R37593. Nucleotides 169
 CC to 382 encode the putative plastid transit peptide, colinear with
 CC and sharing some homology with the transit peptide described for
 CC the Arabidopsis plastid delta-15 glycerolipid desaturase (R37593).
 SQ Sequence 453 AA;

Query Match 8.9%; Score 36; DB 7; Length 453;
 Best Local Similarity 100.0%; Pred. No. 5.93e-44;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dh 327 vtlyhhghedklpwyrgkwsyirglttldrdyg 362
 ||||||||||||||||||||||||||||||||||||
 Qy 277 VTYLHHGHEDKLPWYRGKWSYLRGLTTLDRDYG 312

RESULT 8
 ID R37598 standard; Protein; 156 AA.
 AC R37598;
 DT 01-OCT-1993 (first entry)

DE Sequence of a plastid delta-15 fatty acid.
 KM Lipid composition: modification; fatty acid desaturase; enzyme.
 OS Arabidopsis thaliana, clone pFad3-2 and pFad3p.
 PN M09311245-A.
 PD 10-JUN-1993.
 PE 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: Q43210.

PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure; Page 155; 167pp; English.
 CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. Q43210 is the partial
 CC composite sequence derived from the inserts in plasmids pFad3-2 and
 CC pFad3p. R37598 is a deduced partial peptide sequence of its ORF.
 SQ Sequence 156 AA;

Query Match 7.4%; Score 30; DB 7; Length 156;
 Best Local Similarity 100.0%; Pred. No. 5.28e-34;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dh 95 aggtmfwalltlyghdghsfsndprlnsv 124
 ||||||||||||||||||||||||||||||||||||
 Qy 108 AOGTFMALFVLYGHDCGHSFSDPRLNSV 137

RESULT 9
 ID R60498 standard; Protein; 383 AA.
 AC R60498;
 DT 28-MAR-1995 (first entry)
 DE Linoleic-acid-desaturase; fad3.
 KM Linoleic-acid-desaturase; fad3; oilseed rape; rapeseed;
 KW transgenic plant; crop improvement; yeast artificial chromosome;

KM YAC; linoleic acid.
 OS Brassica napus.
 PN M09418337-A.
 PD 18-AUG-1994.
 PE 04-FEB-1994; U01321.
 PR 05-FEB-1993; US-014431.
 PR 22-NOV-1993; US-156551.
 PA (MONS) MONSANTO CO.
 PA (UNMS) UNIV MICHIGAN STATE.
 PI Amondal VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
 DR WPI: 94-279758/34.
 DR N-PSDB: Q71203

PT Genetically transformed plants with altered linoleic acid
 PT content - contg recombinant, double-stranded DNA encoding
 PT linoleic acid desaturase, or the antisense of the coding
 PT sequence
 PS Disclosure; Page 69-71; 144pp; English.
 CC cDNA encoding the linoleic-acid-desaturase (fad3) of B. napus was
 CC isolated from a YAC library using RFLP 220 and ASA2 markers as
 CC probes. Isolated DNA was amplified using the primers given in
 CC Q71204-09, and used to screen YAC libraries. The fad3 gene was
 CC identified in YAC EW7D11.
 SQ Sequence 383 AA;

Query Match 6.9%; Score 28; DB 11; Length 383;
 Best Local Similarity 100.0%; Pred. No. 1.00e-30;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dh 123 llvpybwtshrtbqnbhqvndesw 150
 ||||||||||||||||||||||||||||||||||||
 Qy 146 ILVPHYGMRLSHRTTHQNHGVNDESW 173

RESULT 10
 ID R37592 standard; Protein; 386 AA.
 AC R37592;
 DT 01-OCT-1993 (first entry)

DE Sequence of delta-15 desaturase.
 KM Lipid composition: modification; fatty acid desaturase; enzyme.
 OS Arabidopsis thaliana, clone pCF3.
 PN M09311245-A.
 PD 10-JUN-1993.
 PE 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: Q43202.

PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure; Page 127-129; 167pp; English.
 CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224.
 SQ Sequence 386 AA;

Query Match 6.9%; Score 28; DB 7; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1.00e-30;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dh 126 llvpybwtshrtbqnbhqvndesw 153
 ||||||||||||||||||||||||||||||||||||
 Qy 146 ILVPHYGMRLSHRTTHQNHGVNDESW 173

RESULT 11
ID R37592 standard; Protein; 380 AA.
AC R37592;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pXf1.
PN W09311245-A.
PD 10-JUN-1993.
PR 03-DEC-1992; U10284.
PE 04-DEC-1991; US-804259.
PI (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, Yadau NS;
DR N-PSDB: 043207.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty acid desaturase or related enzyme with high aminoacid identity to specific polypeptide
PS Disclosure: Page 144-146; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III fragment containing wild-type genomic DNA as a radiolabeled hybridization probe. One of the sequencing primers made to the PCF3 insert was also used. The identity of the expression product of PCF3 as the Arabidopsis microsomal delta-15 desaturase was confirmed by its biological overexpression in plant tissues. Conserved regions of R37592 are useful in designing long oligomers for hybridization as well as shorter ones for use as primers in the PCR. The sequences of useful regions are given in Q43213-Q43224. Arabidopsis delta-15 desaturase cDNA was used as a hybridization probe to isolate a glycerolipid desaturase cDNA from soybean. Plasmid pXf1 was deposited under ATCC 68874.
SQ Sequence 380 AA;
Query Match 6.7%; Score 27; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 4.27e-29;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 295 nihndigtvnhlfqtlphlyeat 321
|||
QY 316 NIHHDIGTHVHLEPQIPHYLVEAT 342
RESULT 12
ID R37597 standard; Protein; 126 AA.
AC R37597;
DT 01-OCT-1993 (first entry)
DE Sequence of an internal region of a corn seed delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Zea mays, clone pPCR20.
PN W09311245-A.
PD 10-JUN-1993.
PR 03-DEC-1992; U10284.
PE 04-DEC-1991; US-804259.
PI (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, Yadau NS;
DR N-PSDB: 043209.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty acid desaturase or related enzyme with high aminoacid identity to specific polypeptide
PS Disclosure: Page 152-153; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III fragment containing wild-type genomic DNA as a radiolabeled hybridization probe. One of the sequencing primers made to the PCF3 insert was also used. The identity of the expression product of PCF3 as the Arabidopsis microsomal delta-15 desaturase was confirmed by its biological overexpression in plant tissues. Conserved regions of

CC R37592 are useful in designing long oligomers for hybridization as well as shorter ones for use as primers in the PCR. The sequences of useful regions are given in Q43213-Q43224. Q43209 is the complete nucleotide sequence of a 396 bp polymerase chain reaction product derived from corn seed mRNA that is found in the insert of plasmid pPCR20. Nucleotides 1 to 31 and 364 to 396 correspond to the amplification primers described in Q43211 and Q43212 respectively. Nucleotides 31 to 363 encode a region that is 61.9% identical to the region between amino acids 137 and 249 of R37591.
SQ Sequence 126 AA;
Query Match 2.2%; Score 9; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 7.93e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 118 vtylhhgh 126
|||
QY 277 VTYLHHGH 285
RESULT 13
ID R53700 standard; Protein; 387 AA.
AC R53700;
DT 09-NOV-1994 (first entry)
DE Sequence of corn microsomal delta-12 desaturase deduced from the cDNA in plasmid pRad2 1.
KW Fatty acid; desaturase; lipid; unsaturated; transgenic plant.
OS Zea mays.
PN W09411516-A.
PD 26-MAY-1994.
PR 15-OCT-1993; U09987.
PE 17-NOV-1992; US-977339.
PI (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Lightner JE, Okuley J;
DR WPI: 94-183515/22.
DR N-PSDB: Q66071.
PT Genes for fatty acid desaturase enzymes - permit alteration of plant lipid composition
PS Claim 13; Page 124-126; 147pp; English.
CC Corn microsomal delta-12 desaturase cDNA was isolated using a PCR approach. A cDNA library was made to poly A+ mRNA from developing corn embryos. This library was used as template for PCR using sets of degenerate oligos NS3 (Q66075) and RB5A/B (Q66077, Q66078) as sense and antisense primers, respectively. NS3 and RB5A/B corresp. to stretches of AAs 101-109 and 318-326, respectively, of R53697, which are conserved in most microsomal delta-12 desaturases. A PCR product of 720bp was purified and used as a probe for screening the corn cDNA library. A plaque was purified and found to encode microsomal delta-12 desaturase truncated at the 3' end. This cDNA was used to probe the corn cDNA library again. The clone congt. CC the longest insert, designated pRad2 1 was sequenced completely (Q66071). An isolated nucleic acid fragment
CC wherein the nucleic acid identity is 90% or greater to CC encoding fatty acid desaturases and related enzymes is claimed CC Q66071 is claimed. A method to isolate nucleic acid fragments which comprises: comparing AA sequences in R53697-R53702 and other CC fatty acid desaturase sequences; identifying conserved sequences of CC 4 or more AAs; designing degenerate oligos based on the conserved CC sequences; and using the oligos to isolate sequences encoding fatty CC acid desaturases and desaturase-related enzymes.
SQ Sequence 387 AA;
Query Match 2.2%; Score 9; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 7.93e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 92 wplywiag 100
|||
QY 102 WPLYWIAG 110
RESULT 14
ID R80294 standard; Protein; 20 AA.

AC R80294:
DT 19-JAN-1996 (first entry)
DE Trehalose releasing enzyme N-terminal fragment.
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriosyltrehalose; alpha-maltotetraosyltrehalose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
OS Arthrobacter sp. Q36.
PN EP-671470-A2.
PD 13-SEP-1995.
PF 07-MAR-1995: 301474.
PR 07-MAR-1994: JP-059840.
PR 07-MAR-1994: JP-059834.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
DR WPI: 95-312772/41.
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
from a non-reducing saccharide having a trehalose structure as an
end unit.
PS Example 4: Page 25; 45pp; English.
CC The trehalose releasing enzyme can be used for the preparation of
CC trehalose with high yields and efficiency from non-reducing
CC saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriosyltrehalose, alpha-maltotetraosyltrehalose and
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
CC This is the N-terminal sequence of the enzyme.
SQ Sequence 20 AA;

Query Match 2.0%; Score 8; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.43e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 eaakpylg 14
|||
OY 343 EAAKPYLG 350

RESULT 15
ID R80290 standard; Protein; 597 AA.
AC R80290:
DT 19-JAN-1996 (first entry)
DE Trehalose releasing enzyme.
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriosyltrehalose; alpha-maltotetraosyltrehalose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
OS Arthrobacter sp. Q36.
PN EP-671470-A2.
PD 13-SEP-1995.
PF 07-MAR-1995: 301474.
PR 07-MAR-1994: JP-059840.
PR 07-MAR-1994: JP-059834.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
DR WPI: 95-312772/41.
DR N-PSDB: Q98670.
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
from a non-reducing saccharide having a trehalose structure as an
end unit.
PS Claim 3: Page 24-25; 45pp; English.
CC This enzyme can be used for the preparation of trehalose with high
CC yields and efficiency from non-reducing saccharides such as
CC alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriosyltrehalose, alpha-maltotetraosyltrehalose and
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
SQ Sequence 597 AA;

Query Match 2.0%; Score 8; DB 14; Length 597;
Best Local Similarity 100.0%; Pred. No. 1.43e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 7 eaakpylg 14
|||
OY 343 EAAKPYLG 350

Search completed: Sat Aug 21 12:31:07 1999
Job time : 115 secs.

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(TM)

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Run on: Sat Aug 21 12:35:11 1999; MasPar time 5.41 Seconds

Tabular output not generated.

Title: >US-09-219-935-9
Description: (1-404) from US09219935.pep
Perfect Score: 404
Sequence: 1 FKFRQSPSPFRRLNSRWMA.....DVYYEADPNLXGEIKYTAE 404

Scoring table: TABLE uniprottable
Gap 60

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 2.765; Variance 0.703; scale 3.933

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	404	100.0	404	3	PCT-US92-1 Sequence 9, Applicatio	0.00e+00
2	378	93.6	378	3	PCT-US92-1 Sequence 7, Applicatio	0.00e+00
3	103	25.5	446	3	PCT-US94-0 Sequence 10, Applicati	2.60e-152
4	103	25.5	446	3	PCT-US92-1 Sequence 5, Applicatio	2.60e-152
5	43	10.6	435	3	PCT-US94-0 Sequence 12, Applicati	1.49e-53
6	36	8.9	453	3	PCT-US93-1 Sequence 13, Applicati	2.37e-42
7	31	7.7	156	3	PCT-US92-1 Sequence 17, Applicati	1.90e-34
8	28	6.9	383	3	PCT-US94-0 Sequence 2, Applicatio	9.34e-30
9	28	6.9	386	3	PCT-US92-1 Sequence 2, Applicatio	9.34e-30
10	27	6.7	380	3	PCT-US92-1 Sequence 11, Applicati	3.34e-28
11	25	6.2	37	2	US-08-320- Sequence 6, Applicatio	4.11e-25
12	25	6.2	37	2	US-08-320- Sequence 22, Applicati	4.11e-25
13	25	6.2	37	1	US-08-314- Sequence 6, Applicatio	4.11e-25
14	25	6.2	37	1	US-08-314- Sequence 22, Applicati	4.11e-25
15	22	5.4	37	1	US-08-314- Sequence 16, Applicati	1.57e-20
16	22	5.4	37	1	US-08-314- Sequence 12, Applicati	1.57e-20
17	22	5.4	37	2	US-08-320- Sequence 16, Applicati	1.57e-20
18	22	5.4	37	2	US-08-320- Sequence 12, Applicati	1.57e-20
19	18	4.5	40	2	US-08-320- Sequence 10, Applicati	1.52e-14
20	18	4.5	40	2	US-08-320- Sequence 18, Applicati	1.52e-14
21	18	4.5	40	1	US-08-314- Sequence 10, Applicati	1.52e-14
22	18	4.5	40	1	US-08-314- Sequence 18, Applicati	1.52e-14
23	12	3.0	37	1	US-08-314- Sequence 26, Applicati	5.32e-06

RESULT	1	STANDARD;	PRT;	404 AA.
ID	PCT-US92-10284-9			
AC	xxxxxx			
XX				
DT				
XX	Sequence 9, Application PC/TUS9210284			
XX				
CC	Sequence 9, Application PC/TUS9210284			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Browne, John, Kinney, Anthony J.,			
CC	APPLICANT: Yadav, Narendra S., Perez-Grau, Luis			
CC	TITLE OF INVENTION: Fatty Acid Desaturase Genes			
CC	TITLE OF INVENTION: from Plants			
CC	NUMBER OF SEQUENCES: 32			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: E. I. du Pont de Nemours and Company			
CC	STREET: 1007 Market Street			
CC	CITY: Wilmington			
CC	STATE: Delaware			
CC	COUNTRY: U.S.A.			
CC	ZIP: 19898			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: Macintosh			
CC	OPERATING SYSTEM: Macintosh System, 6.0			
CC	SOFTWARE: Microsoft Word, 4.0			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: PCT/US92/10284			
CC	FILING DATE: 19921203			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: 07/804,259			
CC	FILING DATE: 4 DECEMBER 1991			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Floyd, Linda A.			
CC	REGISTRATION NUMBER: 33,692			
CC	REFERENCE/DOCKET NUMBER: BB-1036-A			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (302) 992-4929			
CC	TELEFAX: (302) 892-7949			
CC	TELEX: 835420			
CC	INFORMATION FOR SEQ ID NO: 9:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 404 amino acids			

CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
SQ SEQUENCE 404 AA; 46617 MW; 906055 CN;

Query Match 100.0%; Score 404; DB 3; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FKFSQSSPFRRLNSRNMALNTPTPLTVDSSSPPIEEPKTORFGAPPPENLADIR 60
|||||
1 FKFSQSSPFRRLNSRNMALNTPTPLTVDSSSPPIEEPKTORFGAPPPENLADIR 60
QY
61 AAIPIKHCWKNPKMSKSYVVEALIVFALAGAAYLNMMVLWPLWYIAQGMFWALFVLG 120
61 AAIPIKHCWKNPKMSKSYVVEALIVFALAGAAYLNMMVLWPLWYIAQGMFWALFVLG 120
QY
121 HDCGHSFSDPRLSNVGHLHSSILVPIHGMRISRTHNQNHGVNDESNHMPSEKI 180
121 HDCGHSFSDPRLSNVGHLHSSILVPIHGMRISRTHNQNHGVNDESNHMPSEKI 180
QY
121 HDCGHSFSDPRLSNVGHLHSSILVPIHGMRISRTHNQNHGVNDESNHMPSEKI 180
121 HDCGHSFSDPRLSNVGHLHSSILVPIHGMRISRTHNQNHGVNDESNHMPSEKI 180
QY
181 YKSLDKPTREFRFTPLVLAAPPYLWARSFGKSHYHPDSDELPERNDVLTSTACW 240
181 YKSLDKPTREFRFTPLVLAAPPYLWARSFGKSHYHPDSDELPERNDVLTSTACW 240
QY
181 YKSLDKPTREFRFTPLVLAAPPYLWARSFGKSHYHPDSDELPERNDVLTSTACW 240
181 YKSLDKPTREFRFTPLVLAAPPYLWARSFGKSHYHPDSDELPERNDVLTSTACW 240
QY
241 TAMAVALLVCLNFVNGPMQMLKLYIPIYWINVWMLDFVTLHHGHEDKLPYRGKEMSYL 300
241 TAMAVALLVCLNFVNGPMQMLKLYIPIYWINVWMLDFVTLHHGHEDKLPYRGKEMSYL 300
QY
301 RGLGTTLDROYGLNNHHDIGTVIHHLRPOIRPHYLVEATEAKVYLGIKYREPKSG 360
301 RGLGTTLDROYGLNNHHDIGTVIHHLRPOIRPHYLVEATEAKVYLGIKYREPKSG 360
QY
301 RGLGTTLDROYGLNNHHDIGTVIHHLRPOIRPHYLVEATEAKVYLGIKYREPKSG 360
301 RGLGTTLDROYGLNNHHDIGTVIHHLRPOIRPHYLVEATEAKVYLGIKYREPKSG 360
QY
361 PLPLHLGLIAXSIKEDHFVSDGVDVYVEADPNLYGEIKVTAE 404
361 PLPLHLGLIAXSIKEDHFVSDGVDVYVEADPNLYGEIKVTAE 404
QY

RESULT 2
PCT-US92-10284-7 STANDARD; PRT: 378 AA.

Sequence 7, Application PC/TUS9210284
GENERAL INFORMATION:
APPLICANT: Browne, John, Kinney, Anthony J.,
APPLICANT: Pierce, John, Wierzbicki, Anna M.,
APPLICANT: Yadev, Narendra S., Perez-Grau, Luis
TITLE OF INVENTION: Fatty Acid Desaturase Genes
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10284
FILING DATE: 19921203
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/804,259

CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEEX: 835420
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 378 amino acids
CC TYPE: AMINO ACID
CC MOLECULE TYPE: Protein
CC TOPOLOGY: linear
SQ SEQUENCE 378 AA; 43528 MW; 793455 CN;

Query Match 93.6%; Score 378; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LTVDSSSPPIEEPKTORFGAPPPENLADIRAAIPKHCWKNPKMSKSYVVEALIV 60
|||||
1 LTVDSSSPPIEEPKTORFGAPPPENLADIRAAIPKHCWKNPKMSKSYVVEALIV 60
QY
27 LTVDSSSPPIEEPKTORFGAPPPENLADIRAAIPKHCWKNPKMSKSYVVEALIV 60
27 LTVDSSSPPIEEPKTORFGAPPPENLADIRAAIPKHCWKNPKMSKSYVVEALIV 60
QY
61 FALAAGAAYLNMMVLWPLWYIAQGMFWALFVGHDCGHSFSDPRLSNVGHLHSS1 120
61 FALAAGAAYLNMMVLWPLWYIAQGMFWALFVGHDCGHSFSDPRLSNVGHLHSS1 120
QY
87 FALAAGAAYLNMMVLWPLWYIAQGMFWALFVGHDCGHSFSDPRLSNVGHLHSS1 146
87 FALAAGAAYLNMMVLWPLWYIAQGMFWALFVGHDCGHSFSDPRLSNVGHLHSS1 146
QY
121 LVPIHGMRISRTHNQNHGVNDESNHMPSEKIYKSLDKPTREFRFTPLVLAAPPYL 180
121 LVPIHGMRISRTHNQNHGVNDESNHMPSEKIYKSLDKPTREFRFTPLVLAAPPYL 180
QY
147 LVPIHGMRISRTHNQNHGVNDESNHMPSEKIYKSLDKPTREFRFTPLVLAAPPYL 206
147 LVPIHGMRISRTHNQNHGVNDESNHMPSEKIYKSLDKPTREFRFTPLVLAAPPYL 206
QY
181 WASSPGKSGSHYHPDSDELPERNDVLTSTACMTAMAVALLVCLNFVNGPMQMLKLYIPI 240
181 WASSPGKSGSHYHPDSDELPERNDVLTSTACMTAMAVALLVCLNFVNGPMQMLKLYIPI 240
QY
207 WASSPGKSGSHYHPDSDELPERNDVLTSTACMTAMAVALLVCLNFVNGPMQMLKLYIPI 266
207 WASSPGKSGSHYHPDSDELPERNDVLTSTACMTAMAVALLVCLNFVNGPMQMLKLYIPI 266
QY
241 YWINVWMLDFVTLHHGHEDKLPYRGKEMSYLRLGTLTLDROYGLNNHHDIGTVIH 300
241 YWINVWMLDFVTLHHGHEDKLPYRGKEMSYLRLGTLTLDROYGLNNHHDIGTVIH 300
QY
267 YWINVWMLDFVTLHHGHEDKLPYRGKEMSYLRLGTLTLDROYGLNNHHDIGTVIH 326
267 YWINVWMLDFVTLHHGHEDKLPYRGKEMSYLRLGTLTLDROYGLNNHHDIGTVIH 326
QY
301 HHLRPOIRPHYLVEATEAKVYLGIKYREPKSGPLPLHLGLIAXSIKEDHFVSDGVDV 360
301 HHLRPOIRPHYLVEATEAKVYLGIKYREPKSGPLPLHLGLIAXSIKEDHFVSDGVDV 360
QY
327 HHLRPOIRPHYLVEATEAKVYLGIKYREPKSGPLPLHLGLIAXSIKEDHFVSDGVDV 386
327 HHLRPOIRPHYLVEATEAKVYLGIKYREPKSGPLPLHLGLIAXSIKEDHFVSDGVDV 386
QY
361 VYVEADPNLYGEIKVTAE 378
361 VYVEADPNLYGEIKVTAE 378
QY
387 VYVEADPNLYGEIKVTAE 404

RESULT 3
PCT-US94-01321-10 STANDARD; PRT: 446 AA.

Sequence 10, Application PC/TUS9401321
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
NUMBER OF SEQUENCES: 72
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01321
FILING DATE: 04-FEB-1994

CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 446 AA; 51174 MW; 1094717 CN;

Query Match 25.5%; Score 103; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 2,606-152;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPWINVMWLDFTVYLHHGHGDEKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHIDIGTH 366
|||
QY 265 IPWINVMWLDFTVYLHHGHGDEKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHIDIGTH 324
|||
Db 367 VIHHLFPOIPHYHLVEATEAKPVLGKYYRPPDKSGPLPLHL 409
|||
QY 325 VIHHLFPOIPHYHLVEATEAKPVLGKYYRPPDKSGPLPLHL 367
|||

RESULT 4
ID PCT-US92-10284-5 STANDARD; PRT: 446 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 5, Application PC/TUS9210284
XX
CC Sequence 5, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yaday, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 5:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 446 AA; 51174 MW; 1094717 CN;

Query Match 25.5%; Score 103; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 2,606-152;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPWINVMWLDFTVYLHHGHGDEKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHIDIGTH 366
|||
QY 265 IPWINVMWLDFTVYLHHGHGDEKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHIDIGTH 324
|||
Db 367 VIHHLFPOIPHYHLVEATEAKPVLGKYYRPPDKSGPLPLHL 409
|||
QY 325 VIHHLFPOIPHYHLVEATEAKPVLGKYYRPPDKSGPLPLHL 367
|||

RESULT 5
ID PCT-US94-01321-12 STANDARD; PRT: 435 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 12, Application PC/TUS9401321
XX
CC Sequence 12, Application PC/TUS9401321
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
CC TITLE OF INVENTION: in Plants
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 435 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 435 AA; 50136 MW; 1054240 CN;

Query Match 10.6%; Score 43; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,496-53;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 INNHHIDIGTHVIHHLFPOIPHYHLVEATEAKPVLGKYYREP 391
|||
QY 314 INNHHIDIGTHVIHHLFPOIPHYHLVEATEAKPVLGKYYREP 356
|||

RESULT 6
ID PCT-US92-10284-13 STANDARD; PRT: 453 AA.
XX
AC xxxxxx
XX
DT

```

XX DE Sequence 13, Application PC/TUS9210284
CC XX
CC Sequence 13, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 453 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 453 AA; 51362 MW; 1146882 CN;
CC SQ
Query Match 8.9%; Score 36; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.37e-42;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 327 VTYLHHGHEDKLPYRGKEWSYLGRGLTTLDPRDYG 362
|||
Oy 277 VTYLHHGHEDKLPYRGKEWSYLGRGLTTLDPRDG 312
RESULT 7
ID ID PCT-US92-10284-17 STANDARD; PRT; 156 AA.
XX AC xxxxxx
XX XX
DT DT
DE DE
Sequence 17, Application PC/TUS9210284
XX XX
GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC CC

```

```

CC      APRESSEE: E. I. du Pont de Nemours and Company
CC      STREET: 1007 Market Street
CC      CITY: Wilmington
CC      STATE: Delaware
CC      COUNTRY: U.S.A.
CC      ZIP: 19898
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: Macintosh
CC      OPERATING SYSTEM: Macintosh System, 6.0
CC      SOFTWARE: Microsoft Word, 4.0
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US92/10284
CC      FILING DATE: 19921203
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/804,259
CC      FILING DATE: 4 DECEMBER 1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Floyd, Linda A.
CC      REGISTRATION NUMBER: 33,692
CC      REFERENCE/DOCKET NUMBER: BB-1036-A
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (302) 992-4929
CC      TELEFAX: (302) 892-7949
CC      TELEX: 835420
CC      INFORMATION FOR SEQ ID NO: 17:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 156 amino acids
CC      TYPE: AMINO ACID
CC      STRANDEDNESS: unknown
CC      TOPOLOGY: unknown
CC      MOLECULE TYPE: protein
CC      HYPOTHEICAL: YES
CC      FRAGMENT TYPE: N-terminal
CC      ORIGINAL SOURCE:
CC      ORGANISM: Arabidopsis thaliana
CC      IMMEDIATE SOURCE:
CC      CLONE: pRadx-2 and pYac7
CC      SEQUENCE 156 AA; 17771 MW; 128823 CN;
SQ
      Query Match 7.7%; Score 31; DB 3; Length 156;
      Best Local Similarity 100.0%; Pred. No. 1,90e-34;
      Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 126 GHLHSSILVPHGWRISRTHRHONGHVEN 156
      |||||||
QY 139 GHLHSSILVPHGWRISRTHRHONGHVEN 169
      |||||||

RESULT 8
ID PCT-US94-01321-2 STANDARD; PRT; 383 AA.
XX xxxxxx
XX
DT
DE
XX
XX
      Sequence 2, Application PC/TUS9401321
CC
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Lipoenic and Lipoletic Acid Content
CC TITLE OF INVENTION: In Plants
CC NUMBER OF SEQUENCES: 72
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994

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CC	CLASSIFICATION:
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 08/156551
CC	FILING DATE: 22-NOV-1993
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 08/014431
CC	FILING DATE: 05-FEB-1993
CC	INFORMATION FOR SEQ ID NO: 2:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 383 amino acids
CC	TYPE: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
CC	SEQUENCE 383 AA; 43936 MW; 846574 CN;
DB	Query Match 6.9%; Score 28; DB 3; Length 383; Best Local Similarity 100.0%; Pred. No. 9.34e-30; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY	123 ILVPYHGRISHRTHOHNGHVENDSEW 150 146 ILVPYHGRISHRTHOHNGHVENDSEW 173
DE	Sequence 2, Application PC/TUS9210284
XX	Sequence 2, Application PC/TUS9210284
AC	xxxxxx
DT	
CC	GENERAL INFORMATION:
CC	APPLICANT: Browse, John, Kinney, Anthony J.,
CC	APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC	APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC	TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC	TITLE OF INVENTION: from Plants
CC	NUMBER OF SEQUENCES: 32
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: E. I. du Pont de Nemours and Company
CC	STREET: 1007 Market Street
CC	CITY: Wilmington
CC	STATE: Delaware
CC	COUNTRY: U.S.A.
CC	ZIP: 19898
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: floppy disk
CC	COMPUTER: Macintosh
CC	OPERATING SYSTEM: Macintosh System, 6.0
CC	SOFTWARE: Microsoft Word, 4.0
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: PCT/US92/10284
CC	FILING DATE: 19921203
CC	CLASSIFICATION: 435
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: 07/804,259
CC	FILING DATE: 4 DECEMBER 1991
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Floyd, Linda A.
CC	REGISTRATION NUMBER: 33,692
CC	REFERENCE/DOCKET NUMBER: BB-1036-A
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: (302) 992-4929
CC	TELEFAX: (302) 892-7949
CC	TELEX: 835420
CC	INFORMATION FOR SEQ ID NO: 2:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 386 amino acids
CC	TYPE: AMINO ACID
CC	TOPOLOGY: linear

	CC	MOLECULE TYPE:	protein	
SQ	SEQUENCE	386 AA;	44076 MM; 854247 CN;	
		Query Match	6.9%; Score 28;	DB 3;
		Best Local Similarity 100.0%;	Pred. No.	9.34e-30;
	Matches	28;	Conservative	0;
		Mismatches	0;	Indels
		Gaps	0;	
Dd	126	ILVPHGWRISHRTHQHNGHVENDESH	153	
OY	146	ILVPHGWRISHRTHQHNGHVENDESW	173	
RESULT	10	STANDARD;	PRT;	380 AA.
ID	PCT-US92-10284-11			
XX	xxxxxx			
DX				
DT				
Sequence	11,	Application PC/TUS9210284		
DE				
CC	Sequence 11,	Application PC/TUS9210284		
CC	GENERAL INFORMATION:			
CC	APPLICANT:	Browse, John, Kinney, Anthony J.,		
CC	APPLICANT:	Pierce, John, Wierzbicki, Anna M.,		
CC	APPLICANT:	Yadav, Narendra S., Perez-Grau, Luis		
CC	TITLE OF INVENTION:	Fatty Acid Desaturase Genes		
CC	TITLE OF INVENTION:	from Plants		
CC	NUMBER OF SEQUENCES:	32		
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE:	E. I. du Pont de Nemours and Company		
CC	STREET:	1007 Market Street		
CC	CITY:	Wilmington		
CC	STATE:	Delaware		
CC	COUNTRY:	U.S.A.		
CC	ZIP:	19898		
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE:	Floppy disk		
CC	COMPUTER:	Macintosh		
CC	OPERATING SYSTEM:	Macintosh System, 6.0		
CC	SOFTWARE:	Microsoft Word, 4.0		
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER:	PCT/US92/10284		
CC	FILING DATE:	19921203		
CC	CLASSIFICATION:	435		
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER:	07/804,259		
CC	FILING DATE:	4 DECEMBER 1991		
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME:	Floyd, Linda A.		
CC	REGISTRATION NUMBER:	33,692		
CC	REFERENCE/DOCKET NUMBER:	BB-1036-A		
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE:	(302) 992-4929		
CC	TELEX:	835420		
CC	INFORMATION FOR SEQ ID NO:	11:		
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH:	380 amino acids		
CC	TYPE:	AMINO ACID		
CC	TOPOLOGY:	linear		
CC	MOLECULE TYPE:	protein		
SQ	SEQUENCE	380 AA;	44185 MM; 827651 CN;	
	Query Match	6.7%; Score 27;	DB 3;	Length 380;
	Best Local Similarity 100.0%;	Pred. No.	3.34e-28;	
	Matches	27;	Conservative	0;
		Mismatches	0;	Indels
		Gaps	0;	
Dd	295	NINHDIIGHVTIHLFPPQIPHHTVEAT	321	
OY	316	NIHHDIGTIVHIHLFPQIPHHTVEAT	342	

RESULT 11
ID US-08-320-982-6 STANDARD: PRT; 37 AA.
AC xxxxxx
XX
DT
XX Sequence 6, Application US/08320982
DE
XX
CC Sequence 6, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA: 4331 MW: 8403 CN;
SQ
Query Match 6.2%; Score 25; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.11e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIGTIVHHLFPOIPHYHLEAT 25
OY 318 HHDIGTIVHHLFPOIPHYHLEAT 342

RESULT 12
ID US-08-320-982-22 STANDARD: PRT; 37 AA.
AC xxxxxx
XX
DT
XX Sequence 22, Application US/08320982
DE
XX
CC Sequence 22, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:

CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA: 4331 MW: 8403 CN;
SQ
Query Match 6.2%; Score 25; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.11e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIGTIVHHLFPOIPHYHLEAT 25
OY 318 HHDIGTIVHHLFPOIPHYHLEAT 342

RESULT 13
ID US-08-314-596-6 STANDARD: PRT; 37 AA.
AC xxxxxx
XX
DT
XX Sequence 6, Application US/08314596
DE
XX
CC Sequence 6, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-822-0944
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;

Query Match 6.2%; Score 25; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 4,11e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIQTHVHHLFPQIPHYHLEAT 25
QY 318 HHDIQTHVHHLFPQIPHYHLEAT 342

RESULT 14
ID US-08-314-596-22 STANDARD; PRT: 37 AA.
XX xxxxxx
AC
XX
XX
DT
XX
DE Sequence 22, Application US/08314596
CC Sequence 22, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC NUMBER OF SEQUENCES: 48
CC PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DABRY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000

CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;

Query Match 6.2%; Score 25; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 4,11e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIQTHVHHLFPQIPHYHLEAT 25
QY 318 HHDIQTHVHHLFPQIPHYHLEAT 342

RESULT 15
ID US-08-314-596-16 STANDARD; PRT: 37 AA.
XX xxxxxx
AC
XX
XX
DT
XX
DE Sequence 16, Application US/08314596
CC Sequence 16, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC NUMBER OF SEQUENCES: 48
CC PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DABRY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4407 MW; 7119 CN;

Query Match 5.4%; Score 22; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1,57e-20;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIQTHVHHLFPQIPHYHLEAT 22

|||||
Oy 318 HHDICTHVIHHLFOIPIPHLV 339

Search completed: Sat Aug 21 12:35:42 1999
Job time : 31 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit.
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WIDEVIEW (TM)

Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Sat Aug 21 12:42:35 1999; Maspar time 15.98 Seconds
Tabular output not generated. 952.603 Million cell updates/sec

Title: >US-09-219-935-11
Description: (1-380) from US09219935.pep
Perfect Score: 380
Sequence: 1 MWKDTKPLVYANNNGYQOKG.....DTGVDVYXXQFDSLLHSQSD 380

Scoring table: TABLE unitprotatable
Gap 60

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r60
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 3.617; Variance 0.461; scale 7.841

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	380	100.0	380	2	JQ2338	omega-3 fatty acid de	0.00e+00
2	29	7.6	398	2	T01696	omega-3 fatty acid de	2.07e-58
3	29	7.6	441	2	T03029	omega-3 fatty acid de	2.07e-58
4	29	7.6	443	2	T01697	omega-3 fatty acid de	2.07e-58
5	27	7.1	404	2	PQ0812	omega-3 fatty acid de	1.92e-52
6	27	7.1	446	2	JQ2336	omega-3 fatty acid de	1.92e-52
7	27	7.1	453	2	JQ2339	omega-3 fatty acid de	1.92e-52
8	25	6.6	379	2	JC2555	omega-3 fatty acid de	1.53e-46
9	24	6.3	377	2	JQ2337	omega-3 fatty acid de	1.28e-43
10	24	6.3	383	2	A44227	omega-3 fatty acid de	1.28e-43
11	24	6.3	386	2	JQ2335	omega-3 fatty acid de	1.28e-43
12	16	4.2	359	2	S52650	omega-3 fatty acid de	3.71e-21
13	14	4.2	377	2	S73778	MG267 homolog P11.orf	3.75e+00
14	14	4.2	143	2	A70760	hypothetical protein	3.75e+00
15	14	4.2	149	2	B64897	probable membrane pro	3.75e+00
16	14	4.2	168	2	S75746	hypothetical protein	3.75e+00
17	14	4.2	212	2	F71182	hypothetical protein	3.75e+00
18	14	4.2	302	2	B38163	cobv protein - Pseudo	3.75e+00
19	14	4.2	305	2	A70212	conserved hypothetical	3.75e+00
20	14	4.2	312	2	E71624	rifin PRB0055c - mala	3.75e+00
21	14	4.2	316	2	G71600	rifin PRB1005w - mala	3.75e+00
22	14	4.2	326	2	B40141	mitochondrial solute	3.75e+00
23	14	4.2	330	2	JC5717	G protein-coupled rec	3.75e+00

24	7	1.8	357	2	A71523	probable chorismate s	3.75e+00
25	7	1.8	363	2	JC4049	polygalacturonase (EC	3.75e+00
26	7	1.8	376	2	I40728	recombinant protein	3.75e+00
27	7	1.8	400	2	E71338	probable ribose/galac	3.75e+00
28	7	1.8	414	2	S42159	lipotic acid synthase	3.75e+00
29	7	1.8	437	1	B29336	ubiquinol--cytochrome	3.75e+00
30	7	1.8	443	2	B70933	hypothetical protein	3.75e+00
31	7	1.8	445	1	S13869	ubiquinol--cytochrome	3.75e+00
32	7	1.8	473	2	S50755	hypothetical protein	3.75e+00
33	7	1.8	493	2	JC4372	IMP dehydrogenase (EC	3.75e+00
34	7	1.8	504	2	E64118	sodium/proline sympor	3.75e+00
35	7	1.8	513	2	S47788	d-xylose transport AT	3.75e+00
36	7	1.8	555	2	D71444	probable thioesterase	3.75e+00
37	7	1.8	598	2	S65770	maltoicoglycoltrehaos	3.75e+00
38	7	1.8	646	2	S55048	protein-tyrosine kin	3.75e+00
39	7	1.8	698	2	I39713	celb protein - Agrob	3.75e+00
40	7	1.8	727	2	A32561	probable cadmium tran	3.75e+00
41	7	1.8	761	2	D70750	probable ctpa protein	3.75e+00
42	7	1.8	868	2	D69297	transmembrane Oligosa	3.75e+00
43	7	1.8	1101	2	G70951	probable ATP-depend	3.75e+00
44	7	1.8	4544	1	S02392	alpha-2-macroglobulin	3.75e+00
45	6	1.6	449	2	C71216	probable glycine dehy	1.64e+02

ALIGNMENTS

RESULT ENTRY	1	JQ2338	#type complete
TITLE	omega-3 fatty acid desaturase (EC 1.14.99.-) GM3 - soybean		
ORGANISM	#formal_name Glycine max #common_name soybean		
DATE	30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999		

ACCESSIONS	JQ2338
REFERENCE	JQ2338
#authors	Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;

#journal	Peter-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.;
#title	Schweitzer, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
#cross-references	Relfer, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
#accession	Pierce, J.; Browne, J.
#molecule_type	Plant Physiol. (1993) 103:467-476

#residues	1-380 #label YAD
COMMENT	The omega-6 and omega-3 fatty acid desaturases introduce the
	and the third double bonds, respectively, in the biosynthesis of
	18:2 and 18:3 fatty acids, which are important constituents of
	plant membranes.

CLASSIFICATION	#superfamily omega-3 fatty acid desaturase
KEYWORDS	oxidoreductase; transmembrane protein #checksum 1659
SUMMARY	#length 380 #molecular_weight 44185

Query Match	100.0%; Score 380; DB 2; Length 380;
Best local Similarity	100.0%; Pred. No. 0.00e+00;
Matches	380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1 MWKDTKPLVYANNNGYQOKGSSFDPPSPAPPEKIAEIRASIPKHCWKNPWRSLSYLR 60
Qy	
Db	1 MWKDTKPLVYANNNGYQOKGSSFDPPSPAPPEKIAEIRASIPKHCWKNPWRSLSYLR 60
Qy	
Db	61 DWVYIAALVAALAHFPMNLMLTYCPIQGMFALVLDGDCGHSFSSPLNSLVGH 120
Qy	
Db	61 DWVYIAALVAALAHFPMNLMLTYCPIQGMFALVLDGDCGHSFSSPLNSLVGH 120
Qy	
Db	121 LHSLLVPPYHGWRIHRTNHNHGHIEKDESWPLTEKTYKNDSWTRILRFVPPPELV 180
Qy	
Db	121 LHSLLVPPYHGWRIHRTNHNHGHIEKDESWPLTEKTYKNDSWTRILRFVPPPELV 180
Qy	
Db	181 YPIYLSRSPGKSGHFNPNYSNLFPPSEKGAISTLCWATMPSLLIYFSITPLVLK 240
Qy	
Db	181 YPIYLSRSPGKSGHFNPNYSNLFPPSEKGAISTLCWATMPSLLIYFSITPLVLK 240
Qy	

Db	241	LYGIPRYWTFVWMDPVYVYLLHHNGHNOQLPMYRKCKENSYLRGGLTYYDRDGYATYINHDI	300
Qy	241	LYGIPRYWTFVWMDPVYVYLLHHNGHNOQLPMYRKCKENSYLRGGLTYYDRDGYATYINHDI	300
Db	301	GTHVHNLHFPDIPRYHLYVEATOAKPVLGYREPERKSAPLPFLIKYLIQSMRODHFVS	360
Qy	301	GTHVHNLHFPDIPRYHLYVEATOAKPVLGYREPERKSAPLPFLIKYLIQSMRODHFVS	360
Db	361	DTGDVYVYQTDSDLLLSQSD	380
Qy	361	DTGDVYVYQTDSDLLLSQSD	380
RESULT	2	T01696	#type fragment
ENTRY		omega-3 fatty acid desaturase (EC 1.14.99.-)	FAD8 - maize
TITLE		(fragment)	
ORGANISM		#formal_name Zea mays #common_name maize	
DATE		19-Feb-1999	#sequence_revision 19-Feb-1999
ACCESSIONS		T01696	#text_change
REFERENCE		214400	
#authors		Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;	
#journal		Kusano, T.	
#title		Plant Mol. Biol. (1998) 36:297-306	
#accession		Two maize genes encoding omega-3 fatty acid desaturase and their differential expression to temperature.	
#status		T01696	
#molecule_type		preliminary: translated from GB/EMBL/DBJ	
#residues		mRNA	
#cross_references		1-398 #label BER	
#experimental_source		EMBL:D63953; NID:d1164452; PID:d1023305	
GENETICS		#experimental_source strain honey bantum	
#gene		FAD8	
KEYWORDS		oxidoreductase	
SUMMARY		#length 398 #checksum 5580	
Query Match		7.6%; Score 29; DB 2; Length 398;	
Best Local Similarity		100.0%; Pred. No. 2.07e-58;	
Matches		29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	133	VGHILHSILVPYHGWRISRTHQHNGH	161
Qy	117	VGHILHSILVPYHGWRISRTHQHNGH	145
RESULT	3	T03029	#type complete
ENTRY		omega-3 fatty acid desaturase (EC 1.14.99.-)	FAD7 - common tobacco
TITLE		#formal_name Nicotiana tabacum #common_name common tobacco	
ORGANISM		24-Mar-1999	#sequence_revision 24-Mar-1999
DATE		24-Mar-1999	#text_change
ACCESSIONS		T03029	
REFERENCE		214828	
#authors		Hamada, T.; Nishituchi, T.; Kodama, H.; Nishimura, M.; Iba, K.	
#journal		Plant Cell Physiol. (1996) 37:606-611	
#title		CDNA cloning of a wounding-inducible gene encoding a plastid omega-3 fatty acid desaturase from tobacco.	
#accession		T03029	
#status		preliminary: translated from GB/EMBL/DBJ	
#molecule_type		mRNA	
#residues		1-441 #label HAM	
#cross_references		EMBL:D79979; NID:d1093316; PID:g1694625	
#experimental_source		cultivar SRI	
GENETICS		FAD7	
#gene		superfamily omega-3 fatty acid desaturase	
CLASSIFICATION		oxidoreductase	
KEYWORDS		#length 441 #molecular_weight 50310 #checksum 6941	
SUMMARY		7.6%; Score 29; DB 2; Length 441;	
Query Match			

Best Local	Similarity 100.0%;	Pred. No. 2.07e-58;
Matches	29;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	179	VGHILHSSILVPGHGRIISRTTHQNHGH 207
Qy	117	VGHILHSSILVPGHGRIISRTTHQNHGH 145
RESULT	4	
ENTRY	T01697	#type complete
TITLE	omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize	
ORGANISM	#forma_name zea mays #common_name maize	
DATE	19-Feb-1999	#sequence_revision 19-Feb-1999 #text_change 19-Feb-1999
ACCESSIONS	T01697	
REFERENCE	Z14400	
#authors	Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;	
#journal	Kusano, T.	
#file	Plant Mol. Biol. (1998) 36:297-306	
#accession	T01697	Two maize genes encoding omega-3 fatty acid desaturase and their differential expression to temperature.
#status	T01697	Preliminary; translated from GB/EMBL/DBDJ
#molecule_type	DNA	
#residues	1-443	#label BER
#cros-references	EMBL:D63954; NID:d1164453; PID:d1023306	
#experimental_source	strain honey bantum	
GENETICS		
#gene	FAD7	
#introns	163/2; 193/2; 215/3; 246/3; 308/3; 335/3; 381/3	
KEYWORDS	oxidoreductase	
SUMMARY	#length 443	#molecular-weight 49437 #checksum 8872
Query Match	7.6%;	Score 29; DB 2; Length 443;
Best Local	Similarity 100.0%;	Pred. No. 2.07e-58;
Matches	29;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	178	VGHILHSSILVPGHGRIISRTTHQNHGH 206
Qy	117	VGHILHSSILVPGHGRIISRTTHQNHGH 145
RESULT	5	
ENTRY	P00812	#type complete
TITLE	omega-3 fatty acid desaturase (EC 1.14.99.-) BND - rape	
ORGANISM	#forma_name Brassica napus #common_name rape	
DATE	05-Aug-1994	#sequence_revision 05-Aug-1994 #text_change 17-Mar-1999
ACCESSIONS	P00812	
REFERENCE	Q02335	
#authors	Yadav, N.S.; Wierzbicki, A.; Aegegerer, M.; Caster, C.S.;	
	Perer-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;	
	Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;	
	Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;	
	Pierce, J.; Browe, J.	
#journal	Plant Physiol. (1993) 103:467-476	
#file	Cloning of higher plant omega-3 fatty acid desaturases.	
#cros-references	MUTID:94302147	
#contents	CDNA:BND	
#accession	P00812	
#molecule_type	mRNA	
#residues	1-404	#label YAD
#cros-references	GB:I22963	
COMMENT	This enzyme introduces the third double bond in the biosynthesis of	
	18:2 and 18:3 fatty acids which are important constituents of	
	Plant membranes.	
CLASSIFICATION	#superfamily omega-3 fatty acid desaturase	
KEYWORDS	chloroplast; oxidoreductase	
SUMMARY	#length 404	#molecular-weight 46617 #checksum 9400
Query Match	7.1%;	Score 27; DB 2; Length 404;
Best Local	Similarity 100.0%;	Pred. No. 1.92e-52;
Matches	27;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      316 NHHHDIGHVHHLFPOIPHYHLEAT 342
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Oy      295 NHHHDIGHVHHLFPOIPHYHLEAT 321

RESULT      6
ENTRY
TITLE       omega-3 fatty acid desaturase (EC 1.14.99.-) CFD -
            #formal_name Arabidopsis thaliana #common_name mouse-ear
ORGANISM    cress
DATE        30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
           17-Mar-1999
ACCESSIONS  JQ2336
REFERENCE   JQ2335; A49503
AUTHORS     Yadev, N.S.; Wierzbicki, A.; Aegearter, M.; Caster, C.S.;
             Perex-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
             Schweigert, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
             Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
             Piere, J.; Browne, J.
#journal    Plant Physiol. (1993) 103:467-476
#cros-ref   Cloning of higher plant omega-3 fatty acid desaturases.
#accession  JQ2336
#molecule_type mRNA
#residues   1-446 #label YAD

REFERENCE   A49503
AUTHORS     Iba, K.; Gibson, S.; Nishituchi, T.; Fuse, T.; Nishimura, M.;
             Arondel, V.; Hugly, S.; Somerville, C.
#journal    J. Biol. Chem. (1993) 268:24099-24105
#title      A gene encoding a chloroplast omega-3 fatty acid desaturase
             complements alterations in fatty acid desaturation and
             chloroplast copy number of the fad7 mutant of Arabidopsis
             thaliana.
#cros-ref   GenBank accession numbers: X60036, X60037, X60038, X60039,
             X60040, X60041, X60042, X60043, X60044, X60045, X60046,
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#journal      Plant Physiol. (1993) 103:467-476
#title        Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MIMD:94302147
#contents     CDNA:GMD
#accession    JQ2339
##molecule_type mRNA
##residues    1-453 ##label YAD
#cross-references GB:I22965; NID:g408791; PID:g408792
COMMENT       This enzyme introduces the third double bond in the biosynthesis of
              18:2 and 18:3 fatty acids which are important constituents of
              plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS        chloroplast; oxidoreductase
SUMMARY         #length 453 #molecular-weight 51352 #checksum 7549

Query Match          7.1% Score 27; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 1,92e-52;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 366 NIHHDIGTHVHHLFPOIPHYHLYEAT 392
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OY 295 NIHHDIGTHVHHLFPOIPHYHLYEAT 321

RESULT 8
ENTRY JC2555 #type complete
TITLE omega-3 fatty acid desaturase - common tobacco (cv. SR1)
ORGANISM #formal_name Nicotiana tabacum #common_name common tobacco
DATE 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change
24-Sep-1998
ACCESSIONS JC2555
REFERENCE JC2555
AUTHORS Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K.
JOURNAL Gene (1994) 147:293-294
#title Cloning of a cDNA encoding tobacco omega-3 fatty acid
desaturase.
#cross-references MIMD:95011632
#accession JC2535
#status preliminary
##molecule_type mRNA
##residues 1-379 ##label HAM
#cross-references DDBJ:D26509; NID:g1311480; PID:d1006059; PID:g599592
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
SUMMARY #length 379 #molecular-weight 44149 #checksum 1940

Query Match          6.6% Score 25; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.53e-46;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 264 KLPWYRGKEMSYLNGGLTIVDRDYG 288
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OY 267 KLPWYRGKEMSYLNGGLTIVDRDYG 291

RESULT 9
ENTRY JQ2337 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BN3 - rape
ORGANISM #formal_name Brassica napus #common_name rape
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999
ACCESSIONS JQ2337
REFERENCE JQ2335
AUTHORS Yadav, N.S.; Wierzbicki, A.; Aegeleer, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
#journal      Plant Physiol. (1993) 103:467-476
#title        Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MIMD:94302147
#contents     CDNA:BN3
#accession    JQ2337
##molecule_type mRNA

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##residues 1-377 ##label YAD
##cross-references GB:I22962; NID:g408491; PID:g408492
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 377 #molecular-weight 43358 #checksum 3294

Query Match 6.3%; Score 24; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.28e-43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 287 NIHHDIGTHVHLEFPQIPHYHLV 310
|||
295 NIHHDIGTHVHLEFPQIPHYHLV 318

RESULT 10
ENTRY A44227 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - rape
ALTERNATE_NAMES #formal name Brassica napus #common name rape
ORGANISM 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
DATE 20-Mar-1998
ACCESSIONS A44227
REFERENCE A44227
#authors Arcand, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman,
#journal H.M.; Somerville, C.R.
#title Science (1992) 258:1353-1355
#note Map-based cloning of a gene controlling omega-3 fatty acid
#title desaturation in Arabidopsis.
#cross-references MUID:93088059
#accession A44227
##status preliminary: not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-383 ##label ANO
##cross-references GB:I01418; NID:g167147; PID:g167148
#experimental_source developing seed
#note sequence extracted from NCBI backbone (NCBIP:119842)
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 383 #molecular-weight 43936 #checksum 2897

Query Match 6.3%; Score 24; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.28e-43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 293 NIHHDIGTHVHLEFPQIPHYHLV 316
|||
295 NIHHDIGTHVHLEFPQIPHYHLV 318

RESULT 11
ENTRY J02335 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 -
Arabidopsis thaliana
ORGANISM #formal name Arabidopsis thaliana #common name mouse-ear
#cross cress
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
12-Mar-1999
ACCESSIONS J02335; T02487
REFERENCE J02335
#authors Yadev, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reller, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession J02335
#molecule_type mRNA
```

```
##residues 1-386 ##label YAD
REFERENCE 214675
#authors Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
J.C.
#submission submitted to the EMBL Data Library, August 1998
#description Arabidopsis thaliana chromosome II BAC F23f1 genomic
sequence.
#accession T02487
#status translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-386 ##label ROU
##cross-references EMBL:AC004680; NID:g3420043; PID:g3420053
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
GENETICS
#map_position II
#introns 103/2; 133/2; 155/3; 186/3; 248/3; 275/3; 321/3
#note F23f1.10
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 386 #molecular-weight 44076 #checksum 8044

Query Match 6.3%; Score 24; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.28e-43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 296 NIHHDIGTHVHLEFPQIPHYHLV 319
|||
295 NIHHDIGTHVHLEFPQIPHYHLV 318

RESULT 12
ENTRY S52650 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - Synechocystis
sp. (strain PCC6803)
ALTERNATE_NAMES delta 15 desaturase
ORGANISM #formal name Synechocystis sp.
#variety
DATE 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
17-Mar-1999
ACCESSIONS S52650; S75843
REFERENCE S52649
#authors Sakamoto, T.; Los, D.A.; Higashi, S.; Wada, H.; Nishida, I.;
Oimoto, M.; Murata, N.
#journal Plant Mol. Biol. (1994) 26:249-263
#title Cloning of omega-3 desaturase from cyanobacteria and its use
#note in altering the degree of membrane-lipid unsaturation.
#cross-references MUID:95035996
#accession S52650
##molecule_type DNA
##residues 1-359 ##label SAK
##cross-references GB:D13780; NID:g600596; PID:g1003430; PID:g600598
#note the authors translated the initiation codon GTC for
residue 1 as Val

REFERENCE 574322
#authors Kaneo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirosewa, M.; Sugiyara, A.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo,
S.; Takuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.
#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular
cyanobacterium Synechocystis sp. PCC6803. II. Sequence
determination of the entire genome and assignment of
potential protein-coding regions.
#cross-references MUID:97061201
#accession S75843
#status nucleic acid sequence not shown; translation not shown
```


##molecule-type DNA
##residues 1-359 ##label KAN
##cross-references EMBL:D90913; GB:AB001339; NID:g1653348; PID:d1019035;
PID:g1653388
##note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996

GENETICS
#start_codon GTG
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 359 #molecular-weight 41919 #checksum 9162

Query Match 4.28; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 3,71e-21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPHGWRSHRTH 129
QY 125 ILVPHGWRSHRTH 140

RESULT 13
ENTRY S73778 #type complete
TITLE M267 homolog Fil-Orf114 - Mycoplasma pneumoniae (ATCC 29342)
(SGC3)
ORGANISM #formal_name Mycoplasma pneumoniae
#variety ATCC 29342
DATE 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 17-Jul-1998

ACCESSIONS
REFERENCE S73778
#authors Hammelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
#journal Nucleic Acids Res. (1996) 24:4420-4449
#title Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
#cross-references M01D:97105885
#accession S73778
#status preliminary; nucleic acid sequence not shown; translation not shown

##molecule-type DNA
##residues 1-114 ##label HIM
##cross-references EMBL:AE000044; GB:U00089; NID:g1674130; PID:g1674140
##note the nucleotide sequence was submitted to the EMBL Data Library, November 1996

GENETICS
#genetic_code SGC3
SUMMARY #length 114 #molecular-weight 13227 #checksum 9311

Query Match 1.88; Score 7; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.75e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 101 HLIKYL 107
QY 344 HLIKYL 350

RESULT 14
ENTRY A70760 #type complete
TITLE hypothetical protein RV2011c - Mycobacterium tuberculosis (strain H37Rv)
ORGANISM #formal_name Mycobacterium tuberculosis
DATE 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998

ACCESSIONS
REFERENCE A70760
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gas, S.; Barry III, C.E.; Tekait, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jags, K.; Krogh, A.; McLean, J.; Moule, S.;

Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Sgares, R.; Sultson, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
#journal Nature (1998) 393:537-544
#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
#cross-references M01D:98295987
#accession A70760
#status preliminary; nucleic acid sequence not shown; translation not shown

##molecule-type DNA
##residues 1-143 ##label COL
##cross-references GB:Z74025; GB:AL123456; NID:g3261586; PID:e248897;
PID:g1403442
##experimental_source strain H37Rv

GENETICS
#gene RV2011c
SUMMARY #length 143 #molecular-weight 15725 #checksum 8325

Query Match 1.88; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 3.75e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 TSPILVL 93
QY 233 TSPILVL 239

RESULT 15
ENTRY B64897 #type complete
TITLE Probable membrane protein b1447 - Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 13-Nov-1998

ACCESSIONS
REFERENCE B64897
#authors Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.
#journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references M01D:97426617
#accession B64897
#status nucleic acid sequence not shown; translation not shown

##molecule-type DNA
##residues 1-149 ##label BLAT
##cross-references GB:AE000241; GB:U00096; NID:g1787706; PID:g1787718;
#experimental_source strain K-12, substrain MG1655

KEYWORDS
FEATURE
3-19 #domain transmembrane #status predicted #label TM1
34-50 #domain transmembrane #status predicted #label TM2
74-90 #domain transmembrane #status predicted #label TM3
100-116 #domain transmembrane #status predicted #label TM4
128-144 #domain transmembrane #status predicted #label TM5
SUMMARY #length 149 #molecular-weight 15855 #checksum 3006

Query Match 1.88; Score 7; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 3.75e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 39 LINSIVG 45
QY 112 LINSIVG 118

Search completed: Sat Aug 21 12:44:01 1999
Job time : 86 secs.

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Msrch_p protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:44:19 1999; MasPar time 11.15 Seconds

Tabular output not generated. 963.055 Million cell updates/sec

Title: >US-09-219-935-11

Description: (1-380) from US09219935.pep

Perfect Score: 380

Sequence: 1 MYKDTKPLVAAANGYQKQK.....DTGDIVYQTDSLLHSQSD 380

Scoring table: TABLE uniprottable

Gap 60

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot37

1:swissprot

Statistics: Mean 3.684; Variance 0.433; scale 8.502

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	380	100.0	380	1	FD3E_SOYBN OMEGA-3 FATTY ACID DES	0.00e+00
2	29	7.6	447	1	FD3C_SESIN OMEGA-3 FATTY ACID DES	3.13e-63
3	27	7.1	404	1	FD3C_BRANA OMEGA-3 FATTY ACID DES	8.79e-57
4	27	7.1	435	1	FD3D_ARATH TEMPERATURE-SENSITIVE	8.79e-57
5	27	7.1	446	1	FD3C_ARATH OMEGA-3 FATTY ACID DES	8.79e-57
6	27	7.1	453	1	FD3C_SOYBN OMEGA-3 FATTY ACID DES	8.79e-57
7	27	7.1	460	1	FD3C_RICCO OMEGA-3 FATTY ACID DES	8.79e-57
8	25	6.6	379	1	FD3E_TOBAC OMEGA-3 FATTY ACID DES	2.09e-50
9	25	6.6	380	1	FD3E_PHAU OMEGA-3 FATTY ACID DES	2.09e-50
10	24	6.3	377	1	FD3I_BRANA OMEGA-3 FATTY ACID DES	3.01e-47
11	24	6.3	383	1	FD3I_BRANA OMEGA-3 FATTY ACID DES	3.01e-47
12	24	6.3	386	1	FD3E_ARATH OMEGA-3 FATTY ACID DES	3.01e-47
13	21	2.1	217	1	GR04_NEOCA DENSE GRANULE PROTEIN	1.85e-02
14	8	2.1	309	1	HC02_CAEEL PROBABLE 3-HYDROXYACTL	1.85e-02
15	8	1.8	114	1	Y257_MYCN HYPOTHETICAL PROTEIN M	1.77e+00
16	7	1.8	143	1	YW06_MYCTU HYPOTHETICAL 15.7 KD P	1.77e+00
17	7	1.8	149	1	YDCZ_ECOLI HYPOTHETICAL 15.9 KD P	1.77e+00
18	7	1.8	302	1	COB4LAMI15'-PHOSPHAT COBALAMIN 15'	1.77e+00
19	7	1.8	322	1	GDC_RAT GRAVE'S DISEASE CARRIE	1.77e+00
20	7	1.8	330	1	GPA3_HUMAN PUTATIVE G PROTEIN-COU	1.77e+00
21	7	1.8	339	1	RECA_MYCPD RECA PROTEIN.	1.77e+00
22	7	1.8	363	1	PGUR_ASPPA POLYGALACTURONASE PREC	1.77e+00
23	7	1.8	369	1	RECA_CORPS RECA PROTEIN.	1.77e+00

RESULT ID	1	STANDARD	PRT	380 AA.	ALIGNMENTS
AC	PD625	SOYBN	RECA CORGL	RECA PROTEIN.	1.77e+00
DT	01-FEB-1996	(REL. 33, CREATED)	PD62_SOYBN	OMEGA-6 FATTY ACID DES	1.77e+00
DT	01-FEB-1996	(REL. 33, LAST SEQUENCE UPDATE)	PD6E_ARATH	OMEGA-6 FATTY ACID DES	1.77e+00
DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)	PD6E_BRATU	OMEGA-6 FATTY ACID DES	1.77e+00
DE	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).		LIP5_YEAST	LIPIDIC ACID SYNTHETASE	1.77e+00
GN	PD3		CYB_YEAST	CYTOCHROME B (EC 1.10.	1.77e+00
OS	GLYCINE MAX (SOYBEAN).		CYB_RHOCH	CYTOCHROME B (EC 1.10.	1.77e+00
OC	EUKARYOTA; VIRIDIPHYTES; EMBRYOPHYTES; TRACHEOPHYTES;		IMDH_STRPY	INOSINE-5'-MONOPHOSPHA	1.77e+00
CC	EUPHYLLIPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTES; EUDICOTYLEDONS; ROSIDAE;		PUPG_HAEIN	SODIUM/PROLINE SYMPORT	1.77e+00
CC	FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.		XYLG_ECOLI	D-XULOSE TRANSPORT ATP	1.77e+00
NC	[1]		YEB8_SCHPO	HYPOTHETICAL 58.0 KD P	1.77e+00
RP	SEQUENCE FROM N.A.		WEEL_HUMAN	WEEL-LIKE PROTEIN KINA	1.77e+00
RC	TISSUE-SEED:		ROD_MICLU	TRANSCRIPTION TERMINAT	1.77e+00
RX	MEDLINE: 94302147.		CADA_STAAU	PROBABLE CADMIUM-TRANS	1.77e+00
RA	YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,		CPDA_MYCTU	CATION-TRANSPORTING P-	1.77e+00
RA	KINNEY A.J., HIRTZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,		CADD_STAUD	PROBABLE CADMIUM-TRANS	1.77e+00
RA	ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,		AGLU_TETRY	ALPHA-GLUCOSIDASE PREC	1.77e+00
RA	FEIDMANN K.A., PIERCE J., BROWSE J.,		YDF3_SCHPO	PROBABLE EUKARYOTIC IN	1.77e+00
RT	"Cloning of higher plant omega-3 fatty acid desaturases.";		YQ34_BPPI1	LOW-DENSITY LIPOPROTEI	1.77e+00
RL	PLANT PHYSIOL. 103:467-476(1993).		YQ34_BPPI1	HYPOTHETICAL 20.8 KD P	1.77e+00
CC	THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,		YQ34_BPPI1	HYPOTHETICAL 28.2 KD P	1.77e+00
CC	IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE		YQ34_BPPI1	HYPOTHETICAL 75.5 KD P	1.77e+00
CC	CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS				
CC	ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER				
CC	PHOSPHOLIPIDS.				
CC	-1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.				
CC	-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.				
CC	-1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE				
CC	AND/OR BE INVOLVED IN METAL ION BINDING.				
CC	-1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	modified and this statement is not removed. Usage by and for commercial				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: L22964; G408794; -				
DR	PIR: JQ2338; JQ2338				
DR	PIR: PF00487; FA_desaturase; 1.				
DR	OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;				
KW	TRANSMEMBRANE.				

FT	TRANSIT	<1	?	CHLOROPLAST (POTENTIAL).
FT	CHAIN	?	404	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST.
FT	DOMAIN	121	125	HISTIDINE BOX 1.
FT	DOMAIN	157	161	HISTIDINE BOX 2.
FT	DOMAIN	324	328	HISTIDINE BOX 3.
SO	SEQUENCE	404 AA;	46617 MM;	797f19fb CRC32;
Query Match 7.1%; Score 27; DB 1; Length 404;				
Best Local Similarity 100.0%; Pred. No. 8,79e-57;				
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	316	NHHDIGTHVHHLFPQIPHVLVEAT	342	
	295	NHHDIGTHVHHLFPQIPHVLVEAT	321	
RESULT	4	STANDARD:	PRT:	435 AA.
ID	FD3D ARATH			
AC	P46622:			
DT	01-FEB-1996 (REL. 33, CREATED)			
DT	01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)			
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)			
DE	TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST			
DE	PRECURSOR (EC 1.14.99.-).			
CN	FAD8.			
OS	ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).			
OC	EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;			
OC	EUPHYLLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;			
OC	CAPRARALES; BRASSICACEAE; ARABIDOPSIS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CV. COLUMBIA; TISSUE-AERIAL PARTS;			
RC	MEDLINE; 95148742.			
RA	GILSON S., ARONDEL V., IBA K., SOWERVILLE C.R.;			
RT	"Cloning of a temperature-regulated gene encoding a chloroplast			
RT	omega-3 desaturase from Arabidopsis thaliana."			
RL	PLANT PHYSIOL. 106:1615-1621(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;			
RA	MATAHITI M.C. YAMAMOTO K.T.;			
RL	SUBMITTED (SEP.1993) TO EMBL/GENBANK/DBJ DATA BANKS.			
CC	-1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES			
CC	THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY			
CC	ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT			
CC	TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS			
CC	ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.			
CC	-1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.			
CC	-1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).			
CC	-1- INDUCTION: BY LOW TEMPERATURES.			
CC	-1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE			
CC	AND/ OR BE INVOLVED IN METAL ION BINDING.			
CC	-1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; L27158; G516045; -			
DR	EMBL; U08216; G497219; -			
DR	EMBL; D17578; G471093; -			
KW	OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;			
RV	TRANSIT PEPTIDE.			
FT	TRANSIT	1	?	CHLOROPLAST (POTENTIAL).
FT	CHAIN	?	435	TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID
FT	DOMAIN	156	160	DESATURASE, CHLOROPLAST.
FT	DOMAIN	192	196	HISTIDINE BOX 1.
				HISTIDINE BOX 2.

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FT DOMAIN 359 363 HISTIDINE BOX 3.
SQ SEQUENCE 435 AA; 50136 MW; 70613FE0 CRC32;
Query Match 7.1%; Score 27; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 8.79e-57;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 351 NIHHDIGTHVHHLFPQIPHYHLVEAT 377
|||||
0Y 295 NIHHDIGTHVHHLFPQIPHYHLVEAT 321

RESULT 5
AC ID FD3C_ARATH STANDARD; PRT; 446 AA.
P46310;
DT 01-NOV-1995 (REL. 32, CREATED)
DI 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD2 OR FAD2.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC CHLOROPLAST.
OC EUPHYLOTES, VIRIDIPHYTES: STREPTOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES:
OC EUPHYLOTES, SPECIMENOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS: ROSIDAE:
OC CAPPARLES, BRASSICACEAE; ARABIDOPSIS.
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;
RX MEDLINE: 94302147.
RA YADAV N.S., WIERBICKI A., ABERGER M., CASTER C.S., PEREZ-GRU L.,
RA KINNEY A.J., HITE W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-AERIAL PARTS;
RX MEDLINE: 94043239.
RA IBA K., GIBSON S., NISHIMUCHI T., FUSE T., NISHIMURA M., ARONDEL V.,
RA HUGLY S., SOMERVILLE C.R.;
RT "A gene encoding a chloroplast omega-3 fatty acid desaturase
RT complements alterations in fatty acid desaturation and chloroplast
RT copy number of the fad7 mutant of Arabidopsis thaliana.";
RL J. BIOL. CHEM. 268:24099-24105(1993).
[3]
RN RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;
RA WATAHITI M., YANAMOTO K.;
RL SUBMITTED (NOV-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GLYCEROLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L22961; G408481; -
DR EMBL; D14017; G541653; -
DR EMBL; D26019; G468434; -

```

KM	P.FAM: PF00487; FA-desaturase; 1.
DW	OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
RN	TRANSIT PEPTIDE.
FT	TRANSIT ?
FT	CHAIN 1 446 CHLOROPLAST (POTENTIAL), OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST.
FT	DOMAIN 163 167 HISTIDINE BOX 1.
FT	DOMAIN 199 203 HISTIDINE BOX 2.
FT	DOMAIN 366 370 HISTIDINE BOX 3.
SO	SEQUENCE 446 AA; 51174 MW; 8DE08779 CRC32;
Query Match	7.1%; Score 27; DB 1; Length 446;
Best Local Similarity 100.0%;	Pred. No. 8,79e-57;
Matches 27; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Db	358 NIHHDGTHVHHLFPQIPHYALVEAT 384
Oy	295 NIHHDGTHVHHLFPQIPHYALVEAT 321
ID	RESULT 6 STANDARD: PRT; 453 AA.
AC	FD3C_SOYBN P48621;
DT	01-FEB-1996 (REL. 33, CREATED)
DT	01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN	FAD7.
OS	GLYCINE MAX (SOYBEAN).
OC	EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
CC	EUPHYLOTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEONS; ROSIDAE;
CC	FABACEAE; FABACEAE; PAPILIONOIDEAE; GLYCINE.
RN	(1)
RP	SEQUENCE FROM N.A.
RC	TISSUE=SEED;
RX	MEDLINE; 94302147.
RA	YADAV N.S., WIERBICKI A., AGEERTER M., CASTER C.S., PEREZ-GRAU L., ALLEN A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L., KINNEY S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H., FELDMANN K.A., PIERCE J., BROWSE J.;
RA	*Cloning of higher plant omega-3 fatty acid desaturases.*;
RL	PLANT PHYSIOL. 103:467-476(1993).
CC	- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC	- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC	- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLY).
CC	- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/OR BE INVOLVED IN METAL ION BINDING.
CC	- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC	-----
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CC	-----
DR	EMBL; L22965; GA08792; -.
DR	PIR; J02339; J02339.
DR	PFAM; PF00487; FA-desaturase; 1.
DR	OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW	TRANSIT PEPTIDE.
FT	TRANSIT 1.
FT	CHAIN ? 453 CHLOROPLAST (POTENTIAL), OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST.
FT	DOMAIN 171 175 HISTIDINE BOX 1.
FT	DOMAIN 207 211 HISTIDINE BOX 2.
FT	DOMAIN 374 378 HISTIDINE BOX 3.
SO	SEQUENCE 453 AA; 51362 MW; E4314F1B CRC32;

[illegible]

DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
 GN FAD3.
 OS NICOTIANA TABACUM (COMMON TOBACCO).
 OC EUPHAROTIA: VIRIDIPALANAE; STREPTOPHYTA: EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
 CC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; NICOTIANA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. SRL; TISSUE-LEAF;
 RX MEDLINE; 95011632.
 RA HANADA T., KODAMA H., NISHIMURA M., IBA K.:
 RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";
 RL GENE 147:293-294(1994).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D26509; G595992; -.
 DR PFAM; PF00487; FA.desaturase; 1.
 KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 52 72 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT DOMAIN 97 101 HISTIDINE BOX 1.
 FT DOMAIN 133 137 HISTIDINE BOX 2.
 FT DOMAIN 300 304 HISTIDINE BOX 3.
 FT DOMAIN 379 AA; 44149 MW; C237E46D CRC32;
 SQ SEQUENCE 379 AA; 44149 MW; C237E46D CRC32;

 Query Match 6.6%; Score 25; DB 1; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.09e-50;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 264 KLPYRGKMSYLRLGLTVDYDYG 288
 QY 267 KLPYRGKMSYLRLGLTVDYDYG 291

 RESULT 9
 ID FD3E.PHAUV STANDARD; PRT; 380 AA.
 AC P32291;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
 DE (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).
 GN ARG1.
 OS PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).
 OC EUPHAROTIA: VIRIDIPALANAE; STREPTOPHYTA: EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 CC FABALES; FABACEAE; PAPILIONOIDEAE; VIGNA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOCOTYL;
 RA YAMAMOTO K.T., MORI H., IMASEKI H.;

RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
 RT elongating hypocotyls of mung bean (Vigna radiata).";
 RL PLANT CELL PHYSIOL. 33:13-20(1992).
 CC -1- FUNCTION: MICROSOAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D14410; G287562; -.
 DR PFAM; PF00487; FA.desaturase; 1.
 KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 59 78 POTENTIAL.
 FT TRANSMEM 208 231 POTENTIAL.
 FT TRANSMEM 238 256 POTENTIAL.
 FT DOMAIN 97 101 HISTIDINE BOX 1.
 FT DOMAIN 133 137 HISTIDINE BOX 2.
 FT DOMAIN 300 304 HISTIDINE BOX 3.
 FT DOMAIN 380 AA; 43996 MW; 84295F68 CRC32;
 SQ SEQUENCE 380 AA; 43996 MW; 84295F68 CRC32;

 Query Match 6.6%; Score 25; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.09e-50;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 294 HHDIQTHVHHLFQIPHYHLEAVT 318
 QY 297 HHDIQTHVHHLFQIPHYHLEAVT 321

 RESULT 10
 ID FD31.BRANA STANDARD; PRT; 377 AA.
 AC P46311;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
 DE (VERSION 1).
 GN FAD3.
 OS BRASSICA NAPUS (RAPE).
 OC EUPHAROTIA: VIRIDIPALANAE; STREPTOPHYTA: EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 CC CAPPARALES; BRASSICACEAE; BRASSICA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SEED;
 RX MEDLINE; 94302147.
 RA YADAV N.S., WIEZBICKI A., AGERER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMANN K.A., PIERCE J., BROWSE J.:
 RT "Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER

CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -----
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL: L22962; GA08492; -
CC DR PFAM: PF00487; FA-desaturase; 1.
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC TRANSMEMBRANE.
CC FT TRANSMEM 54 73 POTENTIAL.
CC FT TRANSMEM 203 226 POTENTIAL.
CC FT TRANSMEM 233 251 POTENTIAL.
CC FT DOMAIN 92 96 HISTIDINE BOX 1.
CC FT DOMAIN 128 132 HISTIDINE BOX 2.
CC FT DOMAIN 295 299 HISTIDINE BOX 3.
CC SO SEQUENCE 377 AA; 43258 MW; 247237E0 CRC32;
CC -----
CC Query Match 6.3%; Score 24; DB 1; Length 377;
CC Best Local Similarity 100.0%; Pred. No. 3.01e-47;
CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
Cc Db 287 NIHHDIGTWHHLFPQIPHYHLV 310
Cc Qy 295 NIHHDIGTWHHLFPQIPHYHLV 318
Cc |||||||||||||||||||
Cc
Cc RESULT 11
Cc ID FD32_BRANA STANDARD; PRT; 383 AA.
Cc AC P48624;
Cc DT 01-FEB-1996 (REL. 33, CREATED)
Cc DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
Cc DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
Cc DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
Cc DE (VERSION 2).
Cc GN FAD3.
Cc OS BRASSICA NAPUS (RAPE).
Cc OC EUPHAROTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
Cc CC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
Cc CC CAPRIFALES; BRASSICACEAE; BRASSICA.
Cc RN [1]
Cc RP SEQUENCE FROM N.A.
Cc RX MEDLINE: 93088059.
Cc RA ARONDEL V., LEMIEUX B., HNANG I., GIBSON S., GOODMAN H.M.,
Cc RA SOMERVILLE C.R.;
Cc RT "Map-based cloning of a gene controlling omega-3 fatty acid
Cc RT desaturation in Arabidopsis.";
Cc RL SCIENCE 258:1353-1355(1992).
Cc -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
Cc THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
Cc IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
Cc CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
Cc ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
Cc PHOSPHOLIPIDS.
Cc -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
Cc -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
Cc -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
Cc AND/ OR BE INVOLVED IN METAL ION BINDING.
Cc -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
Cc DR EMBL: L01418; G167148; -
Cc DR PFAM: PF00487; FA-desaturase; 1.
Cc KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
Cc TRANSMEMBRANE.
Cc FT TRANSMEM 53 73 POTENTIAL.
Cc FT TRANSMEM 210 230 POTENTIAL.
Cc FT TRANSMEM 234 254 POTENTIAL.
Cc FT DOMAIN 98 102 HISTIDINE BOX 1.
Cc FT DOMAIN 134 138 HISTIDINE BOX 2.
Cc FT DOMAIN 301 305 HISTIDINE BOX 3.
Cc SO SEQUENCE 383 AA; 43936 MW; F39A978B CRC32;
Cc -----
Cc Query Match 6.3%; Score 24; DB 1; Length 383;
Cc Best Local Similarity 100.0%; Pred. No. 3.01e-47;
Cc Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cc -----
Cc Db 293 NIHHDIGTWHHLFPQIPHYHLV 316
Cc Qy 295 NIHHDIGTWHHLFPQIPHYHLV 318
Cc |||||||||||||||||||
Cc
Cc RESULT 12
Cc ID FD32_ARATH STANDARD; PRT; 386 AA.
Cc AC P48623;
Cc DT 01-FEB-1996 (REL. 33, CREATED)
Cc DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
Cc DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
Cc DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
Cc GN FAD3 OR F23F1.10.
Cc OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
Cc OC EUPHAROTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
Cc CC EUPHYLOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTA: EUDICOTYLEDONS; ROSIDAE:
Cc CC CAPRIFALES; BRASSICACEAE; ARABIDOPSIS.
Cc RN [1]
Cc RP SEQUENCE FROM N.A.
Cc RC STRAIN-CV, COLUMBIA; TISSUE=SEEDLING;
Cc RX MEDLINE: 94302147
Cc RA YADAV N.S., WIENZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAD L.,
Cc RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
Cc RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
Cc RA FELDMANN K.A., PIERCE J., BROWSE J.;
Cc RT "Cloning of higher plant omega-3 fatty acid desaturases.";
Cc RL PLANT PHYSIOL. 103:467-476(1993).
Cc [2]
Cc RP SEQUENCE FROM N.A.
Cc RC STRAIN-CV, COLUMBIA; TISSUE=HYPOCOTYL;
Cc RA WATAHIKI M.C., YAMAMOTO K.T.;
Cc RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
Cc RN [3]
Cc RP SEQUENCE FROM N.A.
Cc RC STRAIN-CV, COLUMBIA;
Cc RX MEDLINE: 94345020.
Cc RA NISHICHI T., NISHIMURA M., ARONDEL V., IBA K.;
Cc RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
Cc RT fatty acid desaturase from Arabidopsis thaliana.";
Cc RL PLANT PHYSIOL. 105:767-768(1994).
Cc [4]
Cc RP SEQUENCE FROM N.A.
Cc RC STRAIN-CV, COLUMBIA;
Cc RA ROUNSELEY S.D., LIN X., KENCHUM K.A., CROSBY M.L., BRANDON R.C.,
Cc RA STRES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
Cc RA SOMERVILLE C.R., VENTER J.C.;
Cc RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
Cc -1- FUNCTION: MICROSOAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
Cc THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS
Cc IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
Cc CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
Cc ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
Cc PHOSPHOLIPIDS.

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
OS MYCOPLASMA PNEUMONIAE.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
OC MYCOPLASMATACEAE; MYCOPLASMA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE; 97105885.
RA HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,
RA HERRMANN R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
pneumoniae."
RL NUCLEIC ACIDS RES. 24:4420-4449(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -----
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CC -----
DR EMBL; AE000044; G1674140; -;
KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 75 95 POTENTIAL.
SQ SEQUENCE 114 AA; 13227 MW; 32866BFF CRC32;

Query Match 1.8%; Score 7; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.77e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 101 HLKLYLI 107
Qy 344 HLKLYLI 350

Search completed: Sat Aug 21 12:44:41 1999
Job time : 22 secs.

MIPS RELEASE

(TM)

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MPSrch_DP protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:44:58 1999; MasPar time 22.45 Seconds

Tabular output not generated. 923.998 Million cell updates/sec

Title: >US-09-219-935-11

Description: (1-380) from US09219935.pep

Sequence: 1 MYKDTKPLAYAANNQYQKQ.....DTGDDVYVYQTDLLHSQRD 380

Scoring table: TABLE uniprottable

Gap 60

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: sptrembl9

1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus

Statistics: Mean 3.589; Variance 0.470; scale 7.644

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	32	8.4	436	10	Q40118 DELTA-15 LINEOYL DESAT	9.72e-66
2	29	7.6	398	10	Q24626 FATTY ACID DESATURASE	6.64e-57
3	29	7.6	438	10	P93452 OMEGA-3 FATTY ACID DES	6.64e-57
4	29	7.6	441	10	P93350 OMEGA-3 FATTY ACID DES	6.64e-57
5	29	7.6	443	10	O23824 FATTY ACID DESATURASE	6.64e-57
6	28	7.4	431	10	O82068 W-3 DESATURASE	5.50e-54
7	27	7.1	381	10	P94013 W-3 FATTY ACID DESATUR	4.42e-51
8	27	7.1	407	10	O65792 OMEGA-3 FATTY ACID DES	4.42e-51
9	27	7.1	407	10	O64907 OMEGA-3 DESATURASE (FR	4.42e-51
10	25	6.6	438	10	O04807 OMEGA-3 FATTY ACID DES	2.55e-45
11	21	5.5	380	10	O23802 PLASTID OMEGA-3 FATTY	4.96e-34
12	16	4.2	359	2	O55240 DELTA-15 DESATURASE	1.38e-20
13	11	2.9	350	2	O07872 OMEGA-3 DESATURASE	3.56e-08
14	8	2.1	193	3	O74645 FATTY ACID DESATURASE	8.52e-02
15	7	1.8	64	5	O46248 HUNCHBACK PROTEIN (FRA	5.78e+00
16	7	1.8	152	5	O94519 ACYL-CARRIER SUBUNIT O	5.78e+00
17	7	1.8	186	2	O05332 FOP1 ATP SYNTHASE, SUB	5.78e+00
18	7	1.8	198	2	O46025 IRON REPRESSIBLE POLY	5.78e+00
19	7	1.8	216	5	O25556 GLUTATHIONE S-TRANSFER	5.78e+00
20	7	1.8	257	5	O17734 COSMID C06E7.	5.78e+00

RESULT	ID	1	PRELIMINARY:	PRT:	436 AA.
AC	Q40118				
DT	01-NOV-1996	(TREMBLREL. 01, CREATED)			
DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1999	(TREMBLREL. 09, LAST ANNOTATION UPDATE)			
DE	DELTA-15 LINEOYL DESATURASE.				
OS	LIMNANTHES DOUGLASSII.				
OC	EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:				
OC	EUPHYLLIOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:				
OC	CAPPALES: LIMNANTHACEAE: LIMNANTHES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 95334518.				
RA	BHELLA R.S., MACKENZIE S.L.:				
RT	"Nucleotide sequence of a cDNA from Limnantes douglasii L. encoding				
RT	a delta-15 linoleic acid desaturase."				
RL	PLANT PHYSIOL. 108:861-861(1995).				
DR	EMBL: U17063; G699390; .				
DR	PFAM: PF00487; FA_desaturase; 1.				
DR	MENDEL: 8699; LIMDO:1208:1.				
SO	SEQUENCE 436 AA; 50093 MW; 327D77FE CRC32;				

Query Match 8.4%; Score 32; DB 10; Length 436;
Best Local Similarity 100.0%; Pred. No. 9.72e-66;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

RESULT	ID	2	PRELIMINARY:	PRT:	398 AA.
AC	O24626				
DT	01-JAN-1998	(TREMBLREL. 05, CREATED)			
DT	01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)			
DE	FATTY ACID DESATURASE (FRAGMENT).				
OS	FAD8				
OS	ZEA MAIZE (MAIZE).				
OC	EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:				
OC	EUPHYLLIOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: LILIOPSIDA: POALES;				
OC	POACEAE: ZEA.				

DB 350 NIHHDICGTHVHHPQIPHYHVEATOAPK 381
QY 295 NIHHDICGTHVHHPQIPHYHVEATOAPK 326

[1]
RN SEQUENCE FROM N.A.
RC STRAIN=HONEY BANTAM AND HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
DR EMBL: D84409; D1023307; -;
DR EMBL: D63953; D1023305; -;
DR PFAM; PF00487; FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 398 AA; 44789 MW; 70565EEC CRC32;
Query Match 7.6%; Score 29; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 6,64e-57;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 133 VGHILHSSILVPGHGRISHRTHQNHGH 161
QY 117 VGHILHSSILVPGHGRISHRTHQNHGH 145
RESULT 3
ID P93452 PRELIMINARY; PRT; 438 AA.
AC P93452;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PETROSELINUM CRISPUM (PARSLEY) (PETROSELINUM HORTENSE).
OC EUPHAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; ARALES; APICEAE; PETROSELINUM.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97203190.
RA KIRSCH C., TAKAMIYA-WIK M., REINOLD S., HAHNBROCK K., SOMSSICH I.E.;
RT "Rapid, transient, and highly localized induction of plastidial
RT omega-3 fatty acid desaturase mRNA at fungal infection sites in
RT Petroselinum crispum."
RL PROC. NATL. ACAD. SCI. U.S.A. 94:2079-2084(1997).
DR EMBL; U75745; G1786066; -;
DR PFAM; PF00487; FA_desaturase; 1.
DR MENDEL; 9788; PTCr:1208;1.
SQ SEQUENCE 438 AA; 50391 MW; 9E77A228 CRC32;
Query Match 7.6%; Score 29; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 6,64e-57;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 176 VGHILHSSILVPGHGRISHRTHQNHGH 204
QY 117 VGHILHSSILVPGHGRISHRTHQNHGH 145
RESULT 4
ID P93350 PRELIMINARY; PRT; 441 AA.
AC P93350;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
GN NTFAD7.
OS NICOTIANA TABACUM (COMMON TOBACCO).
OC EUPHAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANACEAE; NICOTIANA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96416425.
RA HANADA T., NISHIOUCHI T., KODAMA H., NISHIMURA M., IBA K.;
RT "CDNA cloning of a wounding-inducible gene encoding a plastid omega-3
RT fatty acid desaturase from tobacco."
RL PLANT CELL PHYSIOL. 37:606-611(1996).
DR EMBL; D79979; D1012141; -;

DR PFAM; PF00487; FA_desaturase; 1.
DR MENDEL; 9312; NICTa:1208;2.
SQ SEQUENCE 441 AA; 50310 MW; 255F96A6 CRC32;
Query Match 7.6%; Score 29; DB 10; Length 441;
Best Local Similarity 100.0%; Pred. No. 6,64e-57;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 179 VGHILHSSILVPGHGRISHRTHQNHGH 207
QY 117 VGHILHSSILVPGHGRISHRTHQNHGH 145
RESULT 5
ID O23824 PRELIMINARY; PRT; 443 AA.
AC O23824;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE.
GN FAD7.
OS ZEA MAYS (MAIZE).
OC EUPHAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
RN [2]
RP SEQUENCE OF 182-443 FROM N.A.
RC STRAIN=HONEY BANTUM;
RX MEDLINE; 98145435.
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RT "Two maize genes encoding omega-3 fatty acid desaturase and their
RT differential expression to temperature."
RL PLANT MOL. BIOL. 36:297-306(1998).
DR EMBL; D63954; D1023306; -;
DR EMBL; D63952; D1023304; -;
DR PFAM; PF00487; FA_desaturase; 1.
SQ SEQUENCE 443 AA; 49437 MW; E8BC6757 CRC32;
Query Match 7.6%; Score 29; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 6,64e-57;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 178 VGHILHSSILVPGHGRISHRTHQNHGH 206
QY 117 VGHILHSSILVPGHGRISHRTHQNHGH 145
RESULT 6
ID O82068 PRELIMINARY; PRT; 431 AA.
AC O82068;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE W-3 DESATURASE.
OS SOLANUM TUBEROSUM (POTATO).
OC EUPHAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANACEAE; SOLANACEAE; SOLANUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DESTREE;
RA LEON J.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DESTREE;
RA MARTIN K.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ007739; E1318202; -
SQ SEQUENCE 431 AA; 49253 MW; BAFAP9CD CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 5,50e-54;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 170 GILHSSILVPHYGWRISHRTHQNHGH 197
118 GILHSSILVPHYGWRISHRTHQNHGH 145

RESULT 7
ID P94013 PRELIMINARY; PRT: 381 AA.

AC 065792;
DT 01-AUG-1998 (TREMBLREL. 03, CREATED)
DT 01-AUG-1998 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE W-3 FATTY ACID DESATURASE.
OS ORYZA SATIVA (RICE).
OC EUPHYLLOPHYTES: SPERMATOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES;
OC EUPHYLLOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: LILIOPSIDA; POALES;
OC POACEAE: TRITICUM.

RP SEQUENCE FROM N.A.
RC STRAIN-IR36, AND NIPPONBARE;
RA AKAGI H.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: D78506; G177376; -
DR EMBL: D78505; G1785856; -
DR MENDEL: 9612; ORISA:1208;1.
SQ SEQUENCE 381 AA; 43640 MW; 2BD4ED6E CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 4.42e-51;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 290 NIHHDIGTVIHHLFPOIPHVLVEAT 316
295 NIHHDIGTVIHHLFPOIPHVLVEAT 321

RESULT 8
ID 065792 PRELIMINARY; PRT: 383 AA.

AC 065792;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
GN TAFAD3.
OS TRITICUM AESTIVUM (WHEAT).
OC EUPHYLLOPHYTES: SPERMATOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES;
OC EUPHYLLOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: LILIOPSIDA; POALES;
OC POACEAE: TRITICUM.

RP SEQUENCE FROM N.A.
RC STRAIN-CV, CHIHOKU; TISSUE-LEAF, AND ROOT;
RA HORIGUCHI G., KAWAKAMI N., KUSUMI K., KODAMA H., IBA K.;
RL PLANT CELL PHYSIOL. 39:540-544(1998).
DR EMBL: D84678; D1029298; -
SQ SEQUENCE 383 AA; 43687 MW; 50D38F40 CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 4.42e-51;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 292 NIHHDIGTVIHHLFPOIPHVLVEAT 318
295 NIHHDIGTVIHHLFPOIPHVLVEAT 321

RESULT 9
ID 064907 PRELIMINARY; PRT: 407 AA.

AC 064907;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)

DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)

DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)

DE OMEGA-3 DESATURASE (FRAGMENT).

GN PXH-15.
OS PELARGONIUM X HORTORUM.
OC EUPHYLLOPHYTES: SPERMATOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES;
OC EUPHYLLOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS; ROSIDAE;
OC GERANIACEAE; PELARGONIUM.

RP SEQUENCE FROM N.A.
RC SCHULTZ D.J., MUMMA R.O., COX-FOSTER D., CRAIG R., MEDFORD J.I.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF020204; G3133289; -
DR NON-TER

SQ SEQUENCE 407 AA; 47169 MW; BC150974 CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 4.42e-51;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 319 NIHHDIGTVIHHLFPOIPHVLVEAT 345
295 NIHHDIGTVIHHLFPOIPHVLVEAT 321

RESULT 10
ID 004807 PRELIMINARY; PRT: 438 AA.

AC 004807;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DE 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PERILLA FRUTESCENS.
OC EUPHYLLOPHYTES: SPERMATOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES;
OC EUPHYLLOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANACEAE; LAMIACEAE; PERILLA.

RP SEQUENCE FROM N.A.
RC STRAIN-OKDONG;
RA LEE S.K., KIM K.H., KIM Y.M., HWANG Y.S.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U59477; G1754795; -
DR PFAM: PF00487; FA.desaturase; 1.
DR MENDEL: 16268; PERFI:1208;tm16268.

SQ SEQUENCE 438 AA; 50160 MW; EF726819 CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.55e-45;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 184 LHSSILVPHYGWRISHRTHQNHGH 208
121 LHSSILVPHYGWRISHRTHQNHGH 145

RESULT 11
ID 023802 PRELIMINARY; PRT: 380 AA.

AC 023802;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PLASTID OMEGA-3 FATTY ACID DESATURASE (FRAGMENT).
GN TAFAD7.
OS TRITICUM AESTIVUM (WHEAT).
OC EUPHYLLOPHYTES: SPERMATOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES;
OC EUPHYLLOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: LILIOPSIDA; POALES;
OC POACEAE: TRITICUM.

RP SEQUENCE FROM N.A.
RC STRAIN-CV, CHIHOKU; TISSUE-LEAF;
RA HORIGUCHI G., IMAKAWA H., KODAMA H., KAWAKAMI N., NISHIMURA M.,

RA IBA K.; PLANTARUM 96:275-283(1996).
RL PHYSIOL. 100:108371; -.
DR EMBL; D43688; D1008371; -.
PFAM; PF00487; FA_desaturase; 1.
FT NON_TER 1 1
SO SEQUENCE 380 AA; 42633 MW; 2123FF56 CRC32;

Query Match 5.5%; Score 21; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 4,96e-34;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 OGTFMALFVLGHDCGHSFS 107
QY 88 OGTFMALFVLGHDCGHSFS 108

RESULT 12
ID 055240; PRELIMINARY; PRT; 359 AA.
AC 055240;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE DELTA 15 DESATURASE.
GN DESB.
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95035996.
RA SAKAMOTO T., LOS D.A., HIGASHI S., WADA H., NISHIDA I., OHMORI M., MURATA N.;
RT "Cloning of omega 3 desaturase from cyanobacteria and its use in altering the degree of membrane-lipid unsaturation.";
RL PLANT MOL. BIOL. 26:249-263(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA TABATA S.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y., MIYAJIMA N., HIROKAWA M., SUGIURA M., SASAMOTO S., KIMURA T., HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NAKUO K., OKUMURA S., SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M., TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
RL DNA RES. 3:109-136(1996).
DR EMBL; D13780; G600598; -.
DR EMBL; D90913; G1653388; -.
PFAM; PF00487; FA_desaturase; 1.
SO SEQUENCE 359 AA; 41919 MW; B5375D98 CRC32;

Query Match 4.2%; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 1,58e-20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPIYHGMWIRSHRTH 129
QY 125 ILVPIYHGMWIRSHRTH 140

RESULT 13
ID 007872; PRELIMINARY; PRT; 350 AA.
AC 007872;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE OMEGA-3 DESATURASE.
GN DESB.
OS SYNECHOCOCUS PCC7002.

OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCOCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97260123.
RA SAKAMOTO T., BRYANT D.A.;
RT "Temperature-regulated mRNA accumulation and stabilization for fatty acid desaturase genes in the cyanobacterium Synechococcus sp. strain PCC 7002.";
RL MOL. MICROBIOL. 23:1281-1292(1997).
DR EMBL; G2197199; -.
PFAM; PF00487; FA_desaturase; 1.
SO SEQUENCE 350 AA; 40562 MW; 969CAD61 CRC32;

Query Match 2.9%; Score 11; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 3,56e-08;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 117 HGMWIRSHRTH 127
QY 130 HGMWIRSHRTH 140

RESULT 14
ID 074645; PRELIMINARY; PRT; 193 AA.
AC 074645;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
OS GIBBERELLA ZEA.
OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
OC HYPOCREALES; HYPOCREACEAE; GIBBERELLA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-P15.
RX MEDLINE; 98433864.
RA KIMURA M., MATSUMOTO G., SHINGU Y., YONEYAMA K., YAMAGUCHI I.;
RT "The mystery of the region around Tril101 and characterization of its RT homologue from Fusarium sporotrichoides.";
RL FEBS LETT. 435:163-168(1998).
DR EMBL; AB014492; D1034743; -.
FT NON_TER 1 1
FT NON_TER 193 193
SO SEQUENCE 193 AA; 21845 MW; BF2053ED CRC32;

Query Match 2.1%; Score 8; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 8,52e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 186 HVIHHLFP 193
QY 303 HVIHHLFP 310

RESULT 15
ID 046248; PRELIMINARY; PRT; 64 AA.
AC 046248;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE HUNCHBACK PROTEIN (FRAGMENT).
OS DROSOPHILA MIMICA (FRUIT FLY) (IDLOMYIA MIMICA).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA; PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RA BAKER R.H., DESALE R.;
RL SYST. BIOL. 46:654-673(1997).
DR EMBL; U93012; G2896866; -.
FT NON_TER 1 1
FT NON_TER 64 64

SQ SEQUENCE 64 AA; 7656 MM; 3A1846DF CRC32;

Query Match 1.8%; Score 7; DB 5; Length 64;

Best Local Similarity 100.0%; Pred. No. 5.78e+00;

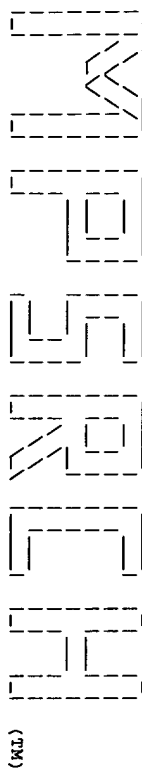
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 HHHGHQ 30

QY 260 HHHGHQ 266

Search completed: Sat Aug 21 12:46:48 1999
Job time : 110 secs.

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(TM)

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March:lp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:38:56 1999; MasPar time 15.00 Seconds

Tabular output not generated. 538.892 Million cell updates/sec

Title: >US-09-219-935-11

Description: (1-380) from US09219935.pep

Sequence: 1 MWKDKPLAAYANNNGYQCKG.....DTGDIVYVYQDTSLHLSQRD 380

Scoring table: TABLE uniprottable

Gap 60

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseqs5

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 2.886; Variance 0.710; scale 4.065

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	287	75.5	380	7	R37595	Sequence of microsoma
2	28	7.4	447	24	W13381	Sesame omega-3 allipha
3	27	7.1	378	7	R37591	Sequence of microsoma
4	27	7.1	404	7	R37594	Sequence of plastid d
5	27	7.1	435	11	R60500	Linoleic-acid-desatur
6	27	7.1	446	11	R60499	Linoleic-acid-desatur
7	27	7.1	446	11	R37593	Sequence of a plastid
8	27	7.1	453	7	R37596	Sequence of soybean P
9	24	6.3	383	11	R60498	Linoleic-acid-desatur
10	24	6.3	386	7	R37592	Sequence of delta-15
11	21	5.5	156	7	R37598	Sequence of a plastid
12	21	5.5	156	7	R37597	Sequence of an intern
13	8	2.1	76	28	W37416	Neospora immunodoma
14	8	2.1	203	28	W31266	Neospora caninum anti
15	8	2.1	231	28	W38262	Gliocladium lipolytic
16	8	2.1	232	28	W38263	Verticillium lipolyti

17	8	2.1	232	28	W38264	Trichophaea saccata 1	1.53e+00
18	7	1.8	20	14	R80294	Trehalose releasing e	2.26e+01
19	7	1.8	224	10	R53701	Sequence of castor mi	2.26e+01
20	7	1.8	302	3	R13512	P dentrificans COB V	2.26e+01
21	7	1.8	330	35	W59906	Human HTADXS50 (G-pro	2.26e+01
22	7	1.8	330	37	W75245	Fragment of human sec	2.26e+01
23	7	1.8	338	17	R90681	B. flavum M7-233 Reca	2.26e+01
24	7	1.8	382	38	W83353	Vernonia galamensis	2.26e+01
25	7	1.8	383	10	R53698	Sequence of microsoma	2.26e+01
26	7	1.8	383	10	R53697	Sequence of microsoma	2.26e+01
27	7	1.8	384	39	W86154	Protein sequence of D	2.26e+01
28	7	1.8	384	39	W86153	Protein sequence of F	2.26e+01
29	7	1.8	384	39	W86155	Protein sequence of D	2.26e+01
30	7	1.8	384	26	W51316	Lesquerella fendleri	2.26e+01
31	7	1.8	384	25	W24997	Microsomal delta-12 f	2.26e+01
32	7	1.8	384	18	R95579	Kappa fatty acid hydr	2.26e+01
33	7	1.8	384	25	W24995	Microsomal delta-12 f	2.26e+01
34	7	1.8	384	25	W24998	Microsomal delta-12 f	2.26e+01
35	7	1.8	384	25	W24996	Microsomal delta-12 f	2.26e+01
36	7	1.8	387	10	R53702	Sequence of castor mi	2.26e+01
37	7	1.8	597	14	R80290	Trehalose releasing e	2.26e+01
38	7	1.8	598	14	R77471	Trehalose releasing e	2.26e+01
39	7	1.8	761	9	R48036	Mycobacterium BCG Imm	2.26e+01
40	7	1.8	4544	9	R47861	Alpha 2-Macroglobulin	2.26e+01
41	7	1.8	4544	11	R60517	Human alpha-2-MR.	2.26e+01
42	6	1.6	209	39	W84171	GNFR-alpha protein f	2.76e+02
43	6	1.6	294	39	W84169	GNFR-alpha protein e	2.76e+02
44	6	1.6	463	39	W84167	GNFR-alpha protein e	2.76e+02
45	6	1.6	463	39	W84165	GNFR-alpha protein e	2.76e+02

ALIGNMENTS

RESULT 1
ID R37595 standard; Protein; 380 AA.
AC R37595;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pxfl.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU POINT DE NEMOURS & CO E.I.
PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR NPI; 93-197063/24.
DR N-PSDB; 043207.
PT Isolated nucleic acid fragment, for plant lipid compn.
PT acid desaturase - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 144-146; 167pp; English.
CC PCR3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCR3
CC insert was also used. The identity of the expression product of PCR3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in 043213-043224. Arabidopsis delta-15
CC desaturase cDNA was used as a hybridization probe to isolate a
CC glycerolipid desaturase cDNA from soybean. Plasmid pxfl was
CC deposited under ATCC 68874.
SQ Sequence 380 AA:
Query Match 75.5%; Score 287; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 94 alf1gndcghsfsdplnslvghlhasllypyngwrishtnqngnhlekdesw 153

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OY 94 ALFLVGHGCGHSEFSDSPLLNSLVGHILHSSLTLYVHGWRISHRHONHGHIEKDESWV 153
DB 154 pltekiynldsmtrllifvypfilylfsrpgkeqshfnpynlfpsserkgia 213
OY 154 PLTEKIYNLDMSMTLIFETVPEFLFVYPIYLFSSPKESGHFNPNLFPSSERKRIA 213
DB 214 lslclwalmfsllylsfitepblvkllygipwylfwmldfvyllhhghqklpwyrg 273
OY 214 ISLCLWALMFSLILYLSFITSPLTLVTKLYGIPWYLFWMVLDVLYLHHGHQKLPWYRG 273
DB 274 kewsylrgltvtddvdywylpnhldictvhlhlfpgqlpghlyveatgaakpvgdyr 333
OY 274 KEWSTLRGGLTVDVDDYWMYVNHHDICTVHNLFPQLPHYHLVEATGAAPVLDGYR 333
DB 334 eperasjpfhnlkylqsmrcqdhfvsdgtgvvyqtdsllhsgrd 380
OY 334 EPERASJPFHNLKYLQSMRQDHFVSDTGVDYVYQTDLSLHSGRD 380

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RESULT 2
ID W13381 standard; Protein; 447 AA.
AC W13381.
DE 02-DEC-1997 (first entry)
KW Sesame omega-3 aliphatic acid desaturase.
KW Sesame; omega-3 aliphatic acid desaturase; modify; fat; oil; plant;
OS Sesamum indicum.
PN J09065882-A.
PD 11-MAR-1997.
PE 01-SEP-1995; 225145.
PR 01-SEP-1995; JP-225145.
PA (TOYA-) TOYAMA KEN.
WP: 97-220417/20.
DR N-PSDB: T62066.
PT Sesame omega-3 aliphatic acid desaturase gene - useful in genetic
engineering to modify fats and oils in agricultural products
PS Claim 6; Page 4; 10pp; Japanese.
CC This protein is a sesame omega-3 aliphatic acid desaturase. Its coding
sequence can be used in genetic engineering to modify fats and oils in
agricultural products. The gene or enzyme can be introduced into a plant
to modify the aliphatic acid composition in its oils and fats, to give
oils and fats with a high content of linolenic acid. Antisense DNA can
be introduced into a plant to inhibit the expression of the gene, so
that oils and fats with little or no linolenic acid are produced. The
CC gene can also be expressed in microorganisms for recombinant production
CC the enzyme.
SQ Sequence 447 AA;

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Query Match 7.4%; Score 28; DB 24; Length 447;
Best Local Similarity 100.0%; Pred. No. 3,89e-30;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 185 ghllhssllvpyhgyrshrchqghh 212
OY 118 GHILHSSILVPHGWRISHRTHQNHGH 145

RESULT 3
ID R37591 standard; Protein; 378 AA.
AC R37591.
DE 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone pBNSF3-f2.
PN W09311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO ) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PT Ydau NS;
DR WPI: 93-197063/24.

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DR N-PSDB: Q43205.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 136-138; 167pp; English.
CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from pCF3 and pCM2 were used to isolate pBNSF3-2. Plasmid pBNSF3-2
CC was deposited as ATCC No. 68854. pBNSF3-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 378 AA;

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Query Match 7.1%; Score 27; DB 7; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.54e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 290 nihndigtvhlhlfpgqlpghlyveat 316
OY 295 NIHNDIGTHVHNLFPQIPHVHLVEAT 321

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RESULT 4
ID R37594 standard; Protein; 404 AA.
AC R37594.
DE 01-OCT-1993 (first entry)
DE Sequence of plastid delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone pBNSF-d-2.
PN W09311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO ) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Ydau NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43206.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 140-141; 167pp; English.
CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from pCF3 and pCM2 were used to isolate pBNSF3-2. Plasmid pBNSF3-2
CC was deposited as ATCC No. 68854. pBNSF3-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 404 AA;

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Query Match 7.1%; Score 27; DB 7; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.54e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 316 nihndigtvhlhlfpgqlpghlyveat 342
OY 295 NIHNDIGTHVHNLFPQIPHVHLVEAT 321

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RESULT 5
ID R60500 standard; Protein; 435 AA.
AC R60500;
DT 28-MAR-1995 (first entry)
DE Lipoic acid desaturase; fadD.
KW Lipoic acid desaturase; fadD; transgenic plant; crop improvement;
OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PE 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS ) MONSANTO CO.
PA (UNMS ) UNIV MICHIGAN STATE.
PI Atonel VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
DR N-PSDB; 071211.
PT Genetically transformed plants with altered lipoic acid
PT content - contg recombinant, double-stranded DNA encoding
PT lipoic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 79-81; 144p; English.
CC The cDNA sequence and deduced amino acid sequence of lipoic-
CC acid-desaturase fadD of Arabidopsis are provided.
SQ Sequence 435 AA;

Query Match 7.1%; Score 27; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.54e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 351 nihdighv1h1ffq4p4hlyeat 377
QY 295 NIHHDIGTHV1H1FFQ4P4HLYEAT 321

RESULT 6
ID R60499 standard; Protein; 446 AA.
AC R60499;
DT 28-MAR-1995 (first entry)
DE Lipoic acid desaturase; fadD.
KW Lipoic acid desaturase; fadD; transgenic plant; crop improvement;
OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PE 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS ) MONSANTO CO.
PA (UNMS ) UNIV MICHIGAN STATE.
PI Atonel VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
DR N-PSDB; 071210.
PT Genetically transformed plants with altered lipoic acid
PT content - contg recombinant, double-stranded DNA encoding
PT lipoic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 75-77; 144p; English.
CC The cDNA sequence and deduced amino acid sequence of lipoic-
CC acid-desaturase fadD of Arabidopsis are provided.
SQ Sequence 446 AA;

Query Match 7.1%; Score 27; DB 11; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.54e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 358 nihdighv1h1ffq4p4hlyeat 384
QY 295 NIHHDIGTHV1H1FFQ4P4HLYEAT 321

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RESULT 7
ID R37593 standard; Protein; 446 AA.
AC R37593;
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone PACF2-2.
PN W09311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; 043204.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 132-134; 167p; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. In contrast to the
CC constitutive expression of the gene encoding (R37592), the mRNA
CC corresponding to Q43204 is abundant in green tissues, rare in roots
CC and leaves, and is about three-fold more abundant in leaf than that
CC of Q43202. R37592 and R37593 show and overall homology of approx.
CC 80%.
SQ Sequence 446 AA;

Query Match 7.1%; Score 27; DB 7; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.54e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 358 nihdighv1h1ffq4p4hlyeat 384
QY 295 NIHHDIGTHV1H1FFQ4P4HLYEAT 321

RESULT 8
ID R37596 standard; Protein; 453 AA.
AC R37596;
DT 01-OCT-1993 (first entry)
DE Sequence of soybean plastid delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pSPD-118bp.
PN W09311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; 043208.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 148-150; 167p; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by

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CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15
CC desaturase cDNA was used as a hybridization probe to isolate a
CC glycerolipid desaturase cDNA from soybean. Plasmid pXFL was
CC deposited under ATCC 68874. Soybean microsomal delta-15
CC desaturase cDNA was used as a hybridization probe to isolate cDNAs
CC encoding related desaturases from soybean. The insert of
CC pSPD-118bp contained a stretch of 1675 nucleotides which contained
CC an open-reading frame encoding a polypeptide (R37596) of about
CC 808 identity with, and colinear with, the Arabidopsis plastid
CC delta-15 desaturase polypeptide listed in R37593. Nucleotides 169
CC to 382 encode the putative plastid transit peptide, colinear with
CC and sharing some homology with the transit peptide described for
CC the Arabidopsis plastid delta-15 glycerolipid desaturase (R37593).
SQ Sequence 453 AA;

Query Match 7.1%; Score 27; DB 7; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.54e-26;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 366 nihndigtvhlhlfpgqiphylveat 392
|||
QY 295 NIHHDIGTHVHLHLPQIPHVHLVAT 321

RESULT 9
ID R60498 standard; Protein; 383 AA.
AC R60498:
DT 28-MAR-1995 (first entry)
DE Linoleic-acid-desaturase fad3.
KW Linoleic-acid-desaturase; fad3; oilseed rape; rapeseed;
KM transgenic plant; crop improvement; yeast artificial chromosome;
KS YAC; linolenic acid.
OS Brassica napus.
PN M09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS.) MONSANTO CO.
PA (UNMS.) UNIV MICHIGAN STATE.
PI Aronoff VJA, Gibson ST, Kishore GM, Ruff TG, Somerville CR;
DR WPI; 94-279758/34.
DR N-PSDB; Q71203.
PT Genetically transformed plants with altered linolenic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoleic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 69-71; 144pp; English.
CC cDNA encoding the linoleic-acid-desaturase (fad3) of B. napus was
CC isolated from a YAC library using RFLP 220 and ASa2 markers as
CC probes. Isolated DNA was amplified using the primers given in
CC Q71204-09, and used to screen YAC libraries. The fad3 gene was
CC identified in YAC EW7D11.
SQ Sequence 383 AA;

Query Match 6.3%; Score 24; DB 11; Length 383;
Best Local Similarity 100.0%; Pred. No. 8.73e-24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 293 nihndigtvhlhlfpgqiphylv 316
|||
QY 295 NIHHDIGTHVHLHLPQIPHVHLV 318

RESULT 10
ID R37592 standard; Protein; 386 AA.
AC R37592:
DT 01-OCT-1993 (first entry)
DE Sequence of delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.

OS Arabidopsis thaliana, clone pCF3.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO.) DU POINT DE MEMOIRS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; Q43202.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 127-129; 167pp; English.
CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Q43210 is the partial
CC composite sequence derived from the inserts in plasmids pFdx-2 and
CC pFdx-7. R37598 is a deduced partial peptide sequence of its ORF.
SQ Sequence 156 AA;

Query Match 5.5%; Score 21; DB 7; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.19e-19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 296 nihndigtvhlhlfpgqiphylv 319
|||
QY 295 NIHHDIGTHVHLHLPQIPHVHLV 318

RESULT 11
ID R37598 standard; Protein; 156 AA.
AC R37598:
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid.
KM Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone pFdx-2 and pFdx-7.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO.) DU POINT DE MEMOIRS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; Q43210.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 155; 167pp; English.
CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Q43210 is the partial
CC composite sequence derived from the inserts in plasmids pFdx-2 and
CC pFdx-7. R37598 is a deduced partial peptide sequence of its ORF.
SQ Sequence 156 AA;

Db 96 ggtmfvalfvghdcghgsfs 116
 |||||||
 QY 88 QGTMFWALFVLGHDCGHGSFS 108

RESULT 12
 ID R37597 standard; Protein; 126 AA.
 AC R37597;
 DT 01-OCT-1993 (first entry)

DE Sequence of an internal region of a corn seed delta-15 desaturase.
 KM Lipid composition: modification; fatty acid desaturase; enzyme.
 OS zea mays; clone pPCR20.
 PN W09311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992: U10284.
 PR 04-DEC-1991: US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E.I.
 PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, Yadao NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: Q43209.

PT Isolated nucleic acid fragment, for plant lipid compn.
 PT modification - comprises nucleic acid sequence encoding fatty acid desaturase or related enzyme with high aminoacid identity to specific polypeptide
 PS Disclosure: Page 152-153; 167pp: English.
 CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III fragment containing wild-type genomic DNA as a radiolabeled hybridization probe. One of the sequencing primers made to the PCR3 insert was also used. The identity of the expression product of PCR3 as the Arabidopsis microsomal delta-15 desaturase was confirmed by its biological overexpression in plant tissues. Conserved regions of CC R37592 are useful in designing long oligomers for hybridization as well as shorter ones for use as primers in the PCR. The sequences of useful regions are given in Q43213-Q43224. Q43209 is the complete nucleotide sequence of a 396 bp polymerase chain reaction product derived from corn seed mRNA that is found in the insert of CC plasmid pPCR20. Nucleotides 1 to 31 and 364 to 396 correspond to CC the amplification primers described in Q43211 and Q43212 respectively. Nucleotides 31 to 363 encode a region that is 61.9% identical to the region between amino acids 137 and 249 of R37591.
 CC Sequence 126 AA;

Query Match 2.4%; Score 9; DB 7; Length 126;
 Best Local Similarity 100.0%; Pred. No. 8,84e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 118 vtylhhgh 126
 |||||||
 QY 256 VTYLHHGH 264

RESULT 13
 ID W37414 standard; Protein; 76 AA.
 AC W37414;
 DT 21-MAY-1998 (first entry)

DE Neospora immunodominant antigen.
 KM Immunodominant antigen; abortion; cattle; infection; diagnosis;
 KW Immunodassay; vaccine; protozoan; parasite.
 OS Neospora sp.
 PN W09742971-A1.
 PD 20-NOV-1997.
 PF 02-MAY-1997: U07500.
 PR 10-MAY-1996: US-645951.
 PA (REGC) UNIV CALIFORNIA.
 PI Anderson ML, Barr BC, Conrad PA, Louie K, Sverlow KW;
 DR WPI: 98-008582/01.
 DR N-PSDB: V00074.

PT DNA encoding immunodominant antigen of bovine Neospora - used in vaccines and in diagnosis of infection
 PS Claim 2; Page 36; 69pp: English.
 CC This protein comprises an immunodominant protein of Neospora that

CC is useful for vaccines and immunodiagnosis of Neospora infection.
 CC The amino acid sequence was deduced from a cDNA clone (see V00074)
 CC isolated from a Neospora bovine strain cDNA library by
 CC immunoscreening with sera from infected cattle. Another
 CC immunodominant protein (see W37413) is also claimed. Also new are:
 CC (1) detection of antibodies (Ab) specific for bovine Neospora
 CC antigen by formation of immune complex between Ab and antigen; (2)
 CC detection of Neospora-specific nucleic acid by hybridisation with a
 CC specific oligonucleotide probe; and (3) a pharmaceutical
 CC composition including bovine Neospora antigen. The methods are
 CC used to diagnose Neospora infection, a major cause of abortion, in
 CC cattle and other animals. Antigens, particularly when expressed by
 CC a recombinant attenuated virus, are used to protect cattle
 CC (especially breeding cows and heifers) against infection.
 CC Sequence 76 AA;

Query Match 2.1%; Score 8; DB 28; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.53e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 laalvaaa 8
 |||||||
 QY 65 IALVAAA 72

RESULT 14
 ID W31266 standard; Protein; 203 AA.
 AC W31266;
 DT 30-APR-1998 (first entry)

DE Neospora caninum antigenic protein Nc4.1.
 KW Neosporosis; antigens; antibodies; mammal; abortion; paralysis.
 OS Neospora caninum.
 PN W09739009-A1.
 PD 23-OCT-1997.
 PF 15-APR-1997: U06285.
 PR 15-APR-1996: US-624677.
 PA (USDA) US SEC OF AGRIC.
 PI Dubley JP, Jenkins MC, Lally NC;
 DR WPI: 97-526385/48.
 DR N-PSDB: T89370.

PT Neospora caninum antigens - useful in assays for diagnosis of neosporosis
 PS Disclosure: Fig 1A; 3pp: English.
 CC This is an antigenic protein (Nc4.1) Neospora from caninum, which
 CC contains at least one epitope capable of detecting antibodies to a
 CC Neospora sp. Neospora sp. causes neosporosis resulting paralysis and
 CC death in dogs and abortion, neonatal morbidity and mortality in sheep,
 CC goats, horses and cattle. The encoded proteins are used in
 CC immunosays (especially ELISA), as reagents for diagnosis of
 CC neosporosis in animals, by detecting antibodies to Neospora sp.
 CC Sequence 203 AA;

Query Match 2.1%; Score 8; DB 28; Length 203;
 Best Local Similarity 100.0%; Pred. No. 1.53e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 128 laalvaaa 135
 |||||||
 QY 65 IALVAAA 72

RESULT 15
 ID W38262 standard; Protein; 231 AA.
 AC W38262;
 DT 11-MAY-1998 (first entry)

DE Glucocladium lipolytic enzyme.
 KW Lipolytic enzyme; lipase; alkalophilic enzyme; detergent;
 KW surfactant; esterification; lipid hydrolysis;
 KW optical isomer resolution.
 OS Glucocladium sp. NR140631 (CBS 173.96).
 FH Key Location/Qualifiers
 FT Peptide 1..31
 /label= sig_peptide

FT Protein 32.231
 FT /label= Mat_protein
 FT /note= "Claim 1"
 PN W09741212-A1.
 PD 06-NOV-1997.
 PF 22-APR-1997; DK0179.
 PR 25-APR-1996; DK-000501.
 PR 25-APR-1996; DK-000500.
 PA (NOVO) NOVO-NORDISK AS.
 PI Borch K, Halkier T, Hirayama S, Nielsen BR, Oxenboll KM,
 PI Sandal T, Talarar;
 DR WPI; 97-549717/50.
 DR N-PSDB; T95844.
 PT Lipolytic enzymes useful as detergent additives at high pH - from
 PT Gliocladium, Verticillium and Trichophaea genera, give good washing
 PT performance and stability in detergent solutions
 PS Claim 1: Page 37-38; 71pp; English.
 CC This protein comprises an alkalophilic lipase from Gliocladium sp.
 CC isolate NMI40631. It is characterised as having lipolytic activity
 CC at pH 10 in the absence of Ca²⁺ above 20% of the activity at pH 10
 CC in the presence of 50 mM Ca²⁺, or giving a degree of hydrolysis
 CC above 15% on cotton/Oil swatches in the Activity-in-Detergent
 CC (AID) assay. The enzyme can be produced by cultivation of the
 CC Gliocladium isolate, or by recombinant production in host cells
 CC utilising an isolated DNA sequence (see T95844). Claimed lipases
 CC (see also W38263 and W38264) can be used as detergent additives
 CC (e.g. as non-dusting granulates, stabilised liquids, slurries or
 CC protected enzymes) to remove lipid or fatty stains, and included
 CC with a surfactant in enzymatic detergent compositions (claimed)
 CC e.g. for laundry and dishwashing, especially at high pH. They are
 CC also useful for interesterification, total hydrolysis of fats and
 CC oils and optical isomer resolution.
 SQ Sequence 231 Aa;

Query Match 2.1%; Score 8; DB 28; Length 231;
 Best Local Similarity 100.0%; Pred. No. 1.53e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 146 aalvaat 153
 |||||
 QY 66 AALVAAA 73

Search completed: Sat Aug 21 12:42:15 1999
 Job time : 199 secs.

NWSEIR (TM)

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Mpsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:47:05 1999; Maspar time 4.95 Seconds

Tabular output not generated. 779.737 Million cell updates/sec

Title: >US-09-219-935-11

Description: (1-380) from US09219935.pep

Perfect Score: 380

Sequence: 1 MWKDKRPLAYANNGYQCKG.....DTGDVYVYQTDLSLLHSQSD 380

Scoring table: TABLE uniprottable

Gap 60

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-issued

1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:Backfiles1

Statistics: Mean 2.726; Variance 0.704; scale 3.871

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	380	100.0	380	3	PCT-US92-1 Sequence 11, Applicati	0.00e+00
2	27	7.1	378	3	PCT-US92-1 Sequence 7, Applicati	7.27e-28
3	27	7.1	404	3	PCT-US92-1 Sequence 9, Applicati	7.27e-28
4	27	7.1	435	3	PCT-US94-0 Sequence 12, Applicati	7.27e-28
5	27	7.1	446	3	PCT-US92-1 Sequence 5, Applicati	7.27e-28
6	27	7.1	446	3	PCT-US94-0 Sequence 10, Applicati	7.27e-28
7	27	7.1	453	3	PCT-US92-1 Sequence 13, Applicati	7.27e-28
8	25	6.6	37	2	US-08-320- Sequence 6, Applicati	8.09e-25
9	25	6.6	37	1	US-08-314- Sequence 6, Applicati	8.09e-25
10	25	6.6	37	1	US-08-314- Sequence 22, Applicati	8.09e-25
11	25	6.6	37	2	US-08-320- Sequence 22, Applicati	8.09e-25
12	25	6.6	156	3	PCT-US92-1 Sequence 17, Applicati	8.09e-25
13	24	6.3	383	3	PCT-US94-0 Sequence 2, Applicati	2.64e-23
14	24	6.3	386	3	PCT-US92-1 Sequence 2, Applicati	2.64e-23
15	22	5.8	37	1	US-08-314- Sequence 16, Applicati	2.67e-20
16	22	5.8	37	1	US-08-314- Sequence 12, Applicati	2.67e-20
17	22	5.8	37	2	US-08-320- Sequence 12, Applicati	2.67e-20
18	22	5.8	37	2	US-08-320- Sequence 12, Applicati	2.67e-20
19	19	5.0	40	2	US-08-320- Sequence 4, Applicati	7.41e-16
20	19	5.0	40	2	US-08-320- Sequence 4, Applicati	7.41e-16
21	19	5.0	40	1	US-08-314- Sequence 4, Applicati	7.41e-16
22	19	5.0	40	1	US-08-314- Sequence 4, Applicati	7.41e-16
23	18	4.7	40	1	US-08-314- Sequence 18, Applicati	2.14e-14

24	18	4.7	40	1	US-08-314- Sequence 10, Applicati	2.14e-14
25	18	4.7	40	2	US-08-320- Sequence 10, Applicati	2.14e-14
26	18	4.7	40	2	US-08-320- Sequence 18, Applicati	2.14e-14
27	14	3.7	37	2	US-08-320- Sequence 26, Applicati	1.07e-08
28	14	3.7	37	2	US-08-320- Sequence 8, Applicati	1.07e-08
29	14	3.7	37	1	US-08-314- Sequence 26, Applicati	1.07e-08
30	14	3.7	37	1	US-08-314- Sequence 8, Applicati	1.07e-08
31	9	2.4	9	3	PCT-US94-0 Sequence 56, Applicati	4.50e-02
32	9	2.4	126	3	PCT-US92-1 Sequence 15, Applicati	4.50e-02
33	8	2.1	8	1	US-08-361- Sequence 8, Applicati	7.33e-01
34	8	2.1	8	2	US-08-789- Sequence 8, Applicati	7.33e-01
35	8	2.1	8	3	PCT-US94-0 Sequence 70, Applicati	7.33e-01
36	8	2.1	8	3	PCT-US94-0 Sequence 63, Applicati	7.33e-01
37	7	1.8	7	3	PCT-US94-0 Sequence 68, Applicati	1.04e+01
38	7	1.8	20	1	US-08-607- Sequence 6, Applicati	1.04e+01
39	7	1.8	24	2	US-08-320- Sequence 14, Applicati	1.04e+01
40	7	1.8	40	1	US-08-314- Sequence 9, Applicati	1.04e+01
41	7	1.8	40	1	US-08-314- Sequence 9, Applicati	1.04e+01
42	7	1.8	40	2	US-08-320- Sequence 23, Applicati	1.04e+01
43	7	1.8	383	2	US-08-320- Sequence 41, Applicati	1.04e+01
44	7	1.8	597	2	US-08-961- Sequence 4, Applicati	1.04e+01
45	7	1.8	761	2	US-08-710- Sequence 2, Applicati	1.04e+01

ALIGNMENTS

RESULT 1
ID PCT-US92-10284-11 STANDARD: PRT: 380 AA.
AC xxxxxx
DT
XX
XX
DE Sequence 11, Application PC/TUS9210284
CC
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 380 amino acids

CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 380 AA; 44185 MW; 827651 CN;

Query Match 100.0%; Score 380; DB 3; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKDKRPLAAYANNGYQOKSGSSFDPSAPPEFKIAETIRASIPKHCWYKMPWRSLSYLR 60
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OY 1 MKDKRPLAAYANNGYQOKSGSSFDPSAPPEFKIAETIRASIPKHCWYKMPWRSLSYLR 60
61 DVLVAALVAAAIHFDNMLMLIYCPICQGTMAFLVGHDCGHSFSDSPILNSLVGHI 120
61 DVLVAALVAAAIHFDNMLMLIYCPICQGTMAFLVGHDCGHSFSDSPILNSLVGHI 120
OY 61 DVLVAALVAAAIHFDNMLMLIYCPICQGTMAFLVGHDCGHSFSDSPILNSLVGHI 120
121 LHSILVPHGKRISHRTHONHGHHEKDESWPLETEKYKNUDSMTLRIRFTVPEPLFV 180
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OY 121 LHSILVPHGKRISHRTHONHGHHEKDESWPLETEKYKNUDSMTLRIRFTVPEPLFV 180
181 YPIYFSRSPGKESGFNFYSMLFPPSEKGIATSLCWATMFSLIYLSFTSPLVLK 240
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OY 181 YPIYFSRSPGKESGFNFYSMLFPPSEKGIATSLCWATMFSLIYLSFTSPLVLK 240
241 LYGIYWFVWMLDVTYIHHGHGOKLPWYRGKEMSYLRGGLTVVDRDYGMIVIHDI 300
|||||
OY 241 LYGIYWFVWMLDVTYIHHGHGOKLPWYRGKEMSYLRGGLTVVDRDYGMIVIHDI 300
301 GTHVHHLPEPQIPHYHLEATQAKPVIGDYYREPERSAPLPFHLIKYLIOSMRDHPVS 360
GTHVHHLPEPQIPHYHLEATQAKPVIGDYYREPERSAPLPFHLIKYLIOSMRDHPVS 360
OY 301 GTHVHHLPEPQIPHYHLEATQAKPVIGDYYREPERSAPLPFHLIKYLIOSMRDHPVS 360
361 DTGDVYVYQTDLSLLHSQRD 380
DTGDVYVYQTDLSLLHSQRD 380
OY 361 DTGDVYVYQTDLSLLHSQRD 380

RESULT 2
ID PCT-US92-10284-7 STANDARD; PRT; 378 AA.
AC xxxxxx
XX
DT
DE
XX
XX
CC Sequence 7, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259

CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 378 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 378 AA; 43528 MW; 793455 CN;

Query Match 7.1%; Score 27; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 7.27e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 290 NIHDIGTHVHHLPEPQIPHYHLEAT 316
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OY 295 NIHDIGTHVHHLPEPQIPHYHLEAT 321

RESULT 3
ID PCT-US92-10284-9 STANDARD; PRT; 404 AA.
AC xxxxxx
XX
XX
DT
XX
DE
XX
XX
CC Sequence 9, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 404 amino acids

CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 08/156551
CC	FILING DATE: 22-NOV-1993
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 08/014431
CC	FILING DATE: 05-FEB-1993
CC	INFORMATION FOR SEQ ID NO: 10:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 446 amino acids
CC	TYPE: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
SQ	SEQUENCE 446 AA; 51174 MW; 1094717 CN;
Dd	Query Match 7.1%; Score 27; DB 3; Length 446; Best Local Similarity 100.0%; Pred.No. 7.27e-28; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	358 NIHHDIGTHTVTHLFPOLIPHYLVLEAT 384 295 NIHHDIGTHTVTHLFPOLIPHYLVLEAT 321
RESULT	7 STANDARD; PRT; 453 AA.
ID	PCT-US92-10284-13
XX	xxxxxx
DE	Sequence 13, Application PC/TUS9210284
XX	Sequence 13, Application PC/TUS9210284
CC	GENERAL INFORMATION:
CC	APPLICANT: Browsee, John, Kinney, Anthony J.,
CC	APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC	APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC	TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC	TITLE OF INVENTION: from Plants
CC	NUMBER OF SEQUENCES: 32
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: E. I. du Pont de Nemours and Company
CC	STREET: 1007 Market Street
CC	CITY: Wilmington
CC	STATE: Delaware
CC	COUNTRY: U.S.A.
CC	ZIP: 19898
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: Macintosh
CC	OPERATING SYSTEM: Macintosh System, 6.0
CC	SOFTWARE: Microsoft Word, 4.0
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: PCT/US92/10284
CC	FILING DATE: 19921203
CC	CLASSIFICATION: 435
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: 07/804,259
CC	FILING DATE: 4 DECEMBER 1991
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Floyd, Linda A.
CC	REGISTRATION NUMBER: 33,692
CC	REFERENCE/DOCKET NUMBER: BB-1036-A
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: (302) 992-4929
CC	TELEFAX: (302) 892-7949
CC	TELEX: 835420
CC	INFORMATION FOR SEQ ID NO: 13:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 453 amino acids
CC	TYPE: AMINO ACID
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein

[illegible]

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XX ID US-08-314-596-6 STANDARD; PRT; 37 AA.
XX AC xxxxxx
XX DT
XX DE
XX SEQUENCE 6, Application US/08314596
CC CC
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC CC
CC CORRESPONDENCE ADDRESSES: 48
CC ADDRESS: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA: 4331 MM; 8403 CN;
SQ
Query Match 6.6%; Score 25; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.09e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHDIETHVHHLFPOIPHYHLEAT 25
QY 297 HHDIETHVHHLFPOIPHYHLEAT 321
RESULT 10
ID US-08-314-596-22 STANDARD; PRT; 37 AA.
XX AC xxxxxx
XX DT
XX DE
XX SEQUENCE 22, Application US/08314596
CC CC
CC Sequence 22, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS

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CC      NUMBER OF SEQUENCES: 48
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC      STREET: 1100 NEW YORK AVENUE, N.W.
CC      CITY: WASHINGTON
CC      STATE: D.C.
CC      COUNTRY: U.S.A.
CC      ZIP: 20005
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/314,596
CC      FILING DATE: 26-SEP-1994
CC      CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: KOKULIS, PAUL N.
CC      REGISTRATION NUMBER: 16,773
CC      REFERENCE/DOCKET NUMBER: 206905/1220
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 202-861-3000
CC      TELEFAX: 202-822-0944
CC      INFORMATION FOR SEQ ID NO: 22:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 37 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: peptide
CC      SEQUENCE 37 AA: 4331 MW: 8403 CN;
SQ
Query Match          6.6%; Score 25; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.09e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHDIQTHVHHLFQIPHYHLYEAT 25
    |||||||||||||||||||
QY 297 HHDIQTHVHHLFQIPHYHLYEAT 321
RESULT 11
STD US-08-320-982-22 STANDARD; PRT; 37 AA.
XX      xxxxxx
XX
DT
XX DE Sequence 22, Application US/08320982
XX
XX DE Patent No. 5801026
CC      GENERAL INFORMATION:
CC      APPLICANT: SOMERVILLE, CHRIS
CC      APPLICANT: VAN DE LOO, FRANK
CC      TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC      TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC      NUMBER OF SEQUENCES: 48
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC      STREET: 1100 NEW YORK AVENUE, N.W.
CC      CITY: WASHINGTON
CC      STATE: D.C.
CC      COUNTRY: U.S.A.
CC      ZIP: 20005
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/320,982

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CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;
SQ

Query Match 6.6%; Score 25; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.09e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIQTHVHHLFPOIPHYHLYEAT 25
|||
OY 297 HHDIQTHVHHLFPOIPHYHLYEAT 321

RESULT 12
ID PCT-US92-10284-17 STANDARD; PRT; 156 AA.
XX
AC xxxxxx
XX
XX
XX
DE Sequence 17, Application PC/TUS9210284
XX
CC Sequence 17, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4829
CC TELEFAX: (302) 892-7949

CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: YES
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Arabidopsis thaliana
CC IMMEDIATE SOURCE:
CC CLONE: pFdx-2 and pYacp7
CC SEQUENCE 156 AA; 17771 MW; 128823 CN;
SQ

Query Match 6.6%; Score 25; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 8.09e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 129 LHSSTLPYHGMRISHRTHQNHG 153
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OY 121 LHSSTLPYHGMRISHRTHQNHG 145

RESULT 13
ID PCT-US94-01321-2 STANDARD; PRT; 383 AA.
XX
AC xxxxxx
XX
XX
XX
XX
DE Sequence 2, Application PC/TUS9401321
XX
CC Sequence 2, Application PC/TUS9401321
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered linolenic and linoleic Acid Content
CC TITLE OF INVENTION: in Plants
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 383 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 383 AA; 43936 MW; 846574 CN;
SQ

Query Match 6.3%; Score 24; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.64e-23;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 293 NIHHDIQTHVHHLFPOIPHYHLY 316
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OY 295 NIHHDIQTHVHHLFPOIPHYHLY 318

RESULT 14

ID PCT-US92-10284-2 STANDARD; PRT; 386 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 2, Application PC/TUS9210284
XX
DE Sequence 2, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browse, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-9929
CC TELEFAX: (302) 892-7949
CC CC TELEEX: 835420
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 386 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 386 AA; 44076 MW; 854247 CN;
SQ
Query Match 6.3%; Score 24; DB 3; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.64e-23;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 296 NIHHDIGTHVHHLFPOIPRHLY 319
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QY 295 NIHHDIGTHVHHLFPOIPRHLY 318
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RESULT 15
ID US-08-314-596-16 STANDARD; PRT; 37 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 16, Application US/08314596
XX
DE Sequence 16, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS

CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4407 MW; 7119 CN;
SQ
Query Match 5.8%; Score 22; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.67e-20;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHHDIGTHVHHLFPOIPRHLY 22
|||
QY 297 HHHDIGTHVHHLFPOIPRHLY 318
|||

Search completed: Sat Aug 21 12:47:17 1999
Job time : 12 secs.

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#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:GMD
#accession JQ2339
##molecule_type mRNA
##residues 1-453 ##label YAD
#cross-references GB:L22965; NID:9408791; PID:9408792
COMMENT This enzyme introduces the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 453 #molecular-weight 51362 #checksum 7549

Query Match 12.7%; Score 16; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 8.02e-23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 320 FVWMLDVTYLHHGH 335
QY 111 FVWMLDVTYLHHGH 126

RESULT 3
ENTRY JQ2337 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BN3 - rape
ORGANISM #formal_name Brassica napus #common_name rape
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

ACCESSIONS JQ2337
REFERENCE JQ2335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:BN3
#accession JQ2337
##molecule_type mRNA
##residues 1-377 ##label YAD
#cross-references GB:L22962; NID:9408491; PID:9408492
COMMENT This enzyme introduces the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 377 #molecular-weight 43258 #checksum 3294

Query Match 7.1%; Score 9; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 248 VTYLHHGH 256
QY 118 VTYLHHGH 126

RESULT 4
ENTRY JQ2338 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GM3 - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

ACCESSIONS JQ2338
REFERENCE JQ2335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;

#journal Pierce, J.; Browne, J.
#title Plant Physiol. (1993) 103:467-476
#cross-references MUID:94302147
#accession JQ2338
##molecule_type mRNA
##residues 1-380 ##label YAD
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second and the third double bonds, respectively, in the biosynthesis of 18:2 and 18:3 fatty acids, which are important constituents of plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase; transmembrane protein
SUMMARY #length 380 #molecular-weight 44185 #checksum 1659

Query Match 7.1%; Score 9; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 256 VTYLHHGH 264
QY 118 VTYLHHGH 126

RESULT 5
ENTRY A44227 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - rape
ALTERNATE_NAMES omega-3 linoleate desaturase
ORGANISM #formal_name Brassica napus #common_name rape
DATE 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

ACCESSIONS A44227
REFERENCE A44227
#authors Arondeil, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman, H.M.; Somerville, C.R.
#journal Science (1992) 258:1353-1355
#title Map-based cloning of a gene controlling omega-3 fatty acid desaturation in Arabidopsis.
#cross-references MUID:93088059
#accession A44227
##status preliminary: not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-383 ##label ARO
#cross-references GB:L01418; NID:g167147; PID:g167148
#experimental_source developing seed
#note sequence extracted from NCBI backbone (NCBIP:119842)
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 383 #molecular-weight 43936 #checksum 2897

Query Match 7.1%; Score 9; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 254 VTYLHHGH 262
QY 118 VTYLHHGH 126

RESULT 6
ENTRY JQ2335 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana
ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear cress
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 12-Mar-1999

ACCESSIONS JQ2335
REFERENCE JQ2335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;

#journal Pierce, J.; Browse, J.
#title Plant Physiol. (1993) 103:467-476
#cross-references EMBL:94302147
#accession J02335
##molecule_type mRNA
##residues 1-386 ##label YAD
REFERENCE
#authors Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
J.C.
#submission submitted to the EMBL Data Library, August 1998
#description Arabidopsis thaliana chromosome II BAC F23F1 genomic
sequence.
#accession T02487
##status translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-386 ##label ROU
##cross-references EMBL:AC004680; NID:g3420043; PID:g3420053
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.

GENETICS
#map_position II
#introns 103/2: 133/2; 155/3; 186/3; 248/3; 275/3; 321/3
#note F23F1.10
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 386 #molecular-weight 44076 #checksum 8044

Query Match 7.1%; Score 9; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 257 VTYLHHGH 265
|||
OY 118 VTYLHHGH 126

RESULT 7
ENTRY T01696 #type fragment
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD8 - maize
ORGANISM (fragment)
#formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
19-Feb-1999

ACCESSIONS
REFERENCE T01696
#authors Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;
Kusano, T.
#journal Plant Mol. Biol. (1998) 36:297-306
#title Two maize genes encoding omega-3 fatty acid desaturase and
their differential expression to temperature.
#accession T01696
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-398 ##label BER
##cross-references EMBL:D63953; NID:d1164452; PID:d1023305
##experimental_source strain honey bantum

GENETICS
#gene FAD8
KEYWORDS oxidoreductase
SUMMARY #length 398 #checksum 5580

Query Match 7.1%; Score 9; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 272 VTYLHHGH 280
|||
OY 118 VTYLHHGH 126

RESULT 8
ENTRY PQ0812 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BND - rape
ORGANISM #formal_name Brassica napus #common_name rape
DATE 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change
17-Mar-1999

ACCESSIONS
REFERENCE PQ0812
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references M01D:94302147
#contents CDNA:BND
#accession PQ0812
##molecule_type mRNA
##residues 1-404 ##label YAD
##cross-references GB:L22963
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 404 #molecular-weight 46617 #checksum 9400

Query Match 7.1%; Score 9; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 277 VTYLHHGH 285
|||
OY 118 VTYLHHGH 126

RESULT 9
ENTRY T01697 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize
ORGANISM #formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
19-Feb-1999

ACCESSIONS
REFERENCE T01697
#authors Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;
Kusano, T.
#journal Plant Mol. Biol. (1998) 36:297-306
#title Two maize genes encoding omega-3 fatty acid desaturase and
their differential expression to temperature.
#accession T01697
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-443 ##label BER
##cross-references EMBL:D63954; NID:d1164453; PID:d1023306
##experimental_source strain honey bantum

GENETICS
#gene FAD7
KEYWORDS oxidoreductase
SUMMARY #length 443 #molecular-weight 49437 #checksum 8872

Query Match 7.1%; Score 9; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 317 VTYLHHGH 325
|||
OY 118 VTYLHHGH 126

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RESULT      10
ENTRY      JQ2336      #type complete
TITLE      omega-3 fatty acid desaturase (EC 1.14.99.-) CFD -
            Arabidopsis thaliana
ORGANISM    #formal name Arabidopsis thaliana #common_name mouse-ear
            cross
DATE        30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
            17-Mar-1999
ACCESSIONS  JQ2336; A49503
REFERENCE   JQ2336
AUTHORS     Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
            Parer-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
            Schmeigler, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
            Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
            Pierce, J.J.; Browne, J.
#journal    Plant Physiol. (1993) 103:467-476
#title      Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MIMD:94302147
#accession  JQ2336
#molecule-type mRNA
#residues   1-446 #label YAD
REFERENCE   A49503
AUTHORS     Iba, K.; Gibson, S.; Nishituchi, T.; Fuse, T.; Nishimura, M.;
            Amondel, V.; Hugly, S.; Somerville, C.
#journal    J. Biol. Chem. (1993) 268:24099-24105
#title      A gene encoding a chloroplast omega-3 fatty acid desaturase
            complements alterations in fatty acid desaturation and
            chloroplast copy number of the fad7 mutant of Arabidopsis
            thaliana.
#cross-references MIMD:94043239
#accession  A49503
#status      preliminary
#molecule-type DNA
#residues    1-446 #label IBA
#cross-references GB:DI4007; NID:9461160; PID:d1003612; PID:9541653
            sequence extracted from NCBI backbone (NCBIN:139485,
            NCBI:139486)
#note        The omega-6 and omega-3 fatty acid desaturases introduce the second
            and the third double bonds, respectively, in the biosynthesis of
            18:2 and 18:3 fatty acids, which are important constituents of
            plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS      oxidoreductase
SUMMARY       #length 446 #molecular_weight 51174 #checksum 4653

Query Match      7.1%; Score 9; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      319 VTYLHHGH 327
QY      118 VTYLHHGH 126

RESULT      11
ENTRY      JC2555
TITLE      omega-3 fatty acid desaturase - common tobacco (cv. SR1)
ORGANISM    #formal_name Nicotiana tabacum #common_name common tobacco
DATE        04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change
            24-Sep-1998
ACCESSIONS  JC2555
REFERENCE   JC2555
AUTHORS     Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal    Gene (1994) 147:293-294
#title      Cloning of a cDNA encoding tobacco omega-3 fatty acid
            desaturase.
#cross-references MIMD:95011632
#accession  JC2555
#status      preliminary
#molecule-type mRNA
#residues    1-379 #label HAM
#cross-references DBJ:DJ26509; NID:g1311480; PID:d1006059; PID:g595952
CLASSIFICATION #superfamily omega-3 fatty acid desaturase

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SUMMARY          #length 379  #molecular-weight 44149  #checksum 1940

Query Match      6.3%; Score 8; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 4,06e-03;
Matches          8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db              253 VTYLHHHG 260
                |||||||
QY             118 VTYLHHHG 125

RESULT          12
ENTRY           S19488  #type complete
TITLE           probable membrane protein YCR073c - yeast (Saccharomyces
                  cerevisiae)
ORGANISM        #formal_name Saccharomyces cerevisiae
DATE            31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
                  19-Dec-1997

ACCESSIONS     S19488
REFERENCE       S19486
                S19488
#authors        Ballestra, J.P.G.; Franco, L.; Hoenicka, J.; Jimenez, A.;
#submission     submitted to the Protein Sequence Database, March 1992
#accession      S19488
#molecule_type DNA
#residues       1-1314 ##label BAL
#cross-references EMBL:X59720; NID:g1907116; PID:e264558; PID:g1907212;
                MIPS:YCR073c

GENETICS
#map_position 3R
CLASSIFICATION  #superfamily unassigned Ser/Thr or Tyr-specific protein
                  kinases; protein kinase homology
KEYWORDS        serine/threonine-specific protein kinase; transmembrane
                  protein

FEATURE
390-405          #domain transmembrane #status predicted #label TM1\
462-478          #domain transmembrane #status predicted #label TM2\
718-735          #domain transmembrane #status predicted #label TM3\
875-892          #domain transmembrane #status predicted #label TM4\
937-953          #domain transmembrane #status predicted #label TM5\
1032-1310        #domain protein kinase homology #label KIN\
1040-1048        #region protein kinase ATP-binding motif
SUMMARY         #length 1314 #molecular-weight 150634 #checksum 4169

Query Match      6.3%; Score 8; DB 2; Length 1314;
Best Local Similarity 100.0%; Pred. No. 4,06e-03;
Matches          8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db              390 LLAPPYVL 397
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QY             40 LLAPPYVL 47

RESULT          13
ENTRY           H69057  #type complete
TITLE           hypothetical protein MTH134 - Methanobacterium
                  thermoautotrophicum (strain Delta H)
ORGANISM        #formal_name Methanobacterium thermoautotrophicum
DATE            05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
                  05-Jun-1998

ACCESSIONS     H69057
REFERENCE       H69057
#authors        Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.;
                  Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.;
                  Cook, R.; Gilbert, K.; Harrison, D.; Hong, L.; Keagle, P.;
                  Lumma, W.; Pothier, B.; Qiu, D.; Spadefora, R.; Vicaire, R.;
                  Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Caruso,
                  A.; Bush, D.; Saffer, H.; Patwell, D.; Prabhakar, S.;
                  McDougall, S.; Shimer, G.; Goyal, A.; Pietrovski, S.;
                  Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling,
                  J.; Reeve, J.N.
J. Bacteriol. (1997) 179:7135-7155
Complete genome sequence of Methanobacterium

```

thermoautotrophicum Delta H: functional analysis and
comparative genomics.
#cross-references MUID:98037514
#accession H69057
#status preliminary: nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-254 ##label MTH
##cross-references GB:AE000905; GB:AE000666; NID:g2622541; PID:g2622546
##experimental_source strain Delta H

GENETICS
#gene MTH434
#start_codon GTG
SUMMARY #length 254 #molecular-weight 28253 #checksum 3627

Query Match 5.6%; Score 7; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.08e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 220 YGIPYLV 226
|||
QY 104 YGIPYLV 110

RESULT 14
ENTRY A71351 #type complete
TITLE probable cobalt ABC transporter, ATP-binding protein -
ORGANISM syphilis spirochete
#format_name Treponema pallidum subsp. pallidum #common_name
syphilis spirochete
DATE 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
17-Mar-1999

ACCESSIONS
REFERENCE A71351
#authors Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.;
Sutton, G.G.; Dodson, R.; Gwin, M.; Hickey, E.K.; Clayton,
R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod,
M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson,
D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDonald,
L.; Artach, P.; Bowman, C.; Cotton, M.D.; Fujii, C.;
Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Wathey,
L.; Weidman, J.; Smith, H.O.; Venter, J.C.
#journal Science (1998) 281:375-388
#title Complete genome sequence of Treponema pallidum, the syphilis
spirochete.
#cross-references MUID:98332770
#accession A71351
#status preliminary: nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-255 ##label COL
##cross-references GB:AE001204; GB:AE000520; NID:g3322492; PID:g3322495
##experimental_source strain Nichols

GENETICS
#gene TP0227
CLASSIFICATION #superfamily ATP-binding cassette homology
FEATURE 35-217 #domain ATP-binding cassette homology #label ABC
SUMMARY #length 255 #molecular-weight 27321 #checksum 8819

Query Match 5.6%; Score 7; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.08e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 104 CAFCPLQ 110
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QY 93 CAFCPLQ 99

RESULT 15
ENTRY A64763 #type complete
TITLE probable transport protein mhpT - Escherichia coli
ORGANISM #format_name Escherichia coli

DATE 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
13-Nov-1998

ACCESSIONS
REFERENCE A64763
#authors Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
Y.
#journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
#accession A64763
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-418 ##label BLAT
##cross-references GB:AE000142; GB:U00096; NID:g1786542; PID:g1786549;
DMGP:b0353

GENETICS
##experimental_source strain K-12, substrain MG1655

KEYWORDS mhpT
FEATURE transmembrane protein; transport protein

28-44 #domain transmembrane #status predicted #label TM1
73-89 #domain transmembrane #status predicted #label TM2
97-113 #domain transmembrane #status predicted #label TM3
126-142 #domain transmembrane #status predicted #label TM4
155-171 #domain transmembrane #status predicted #label TM5
185-201 #domain transmembrane #status predicted #label TM6
234-250 #domain transmembrane #status predicted #label TM7
299-315 #domain transmembrane #status predicted #label TM8
390-406 #domain transmembrane #status predicted #label TM9

SUMMARY #length 418 #molecular-weight 43417 #checksum 3578

Query Match 5.6%; Score 7; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 4.08e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 305 MSLSLA 311
|||
QY 84 MSLSLA 90

Search completed: Sat Aug 21 12:51:23 1999
Job time : 22 secs.

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FT	CHAIN	?	453	OMEGA-3 FATTY ACID DESATURASE
FT	DOMAIN	171	175	CHOROPLAST.
FT	DOMAIN	207	211	HISTIDINE BOX 1.
FT	DOMAIN	374	378	HISTIDINE BOX 2.
SO	SEQUENCE	453 AA:	51362 MW:	HISTIDINE BOX 3. E4314FLB CMC32?

Query Match	12.7%	Score 16;	DB 1;	Length 453;
Best Local Similarity	100.0%	Pred. No. 6.08e-25;		
Matches	16;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

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Db      320 EVMWLDVTVLHHNGH 335
        |||
QY      111 EVMWLDVTVLHHNGH 126

```

RESULT	2	STANDARD;	PRT;	447	AA
ID	FD3C_SESIN				
1	04830				

DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-)

0C EUKARYOTA: VIRIDIPLANTAE: EMBRYOPHYTA: TRACHEOPHYTA
0C EUKARYOTA: VIRIDIPLANTAE: EMBRYOPHYTA: TRACHEOPHYTA
0C EUPHYLLIPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS:
0C ASTERIDAE: GENTIANANAE: LAMIALES: PEDALIACEAE: SESAMUM.

RC STRAIN=CV. 4294; TISSUE=COTYLEDON;
RA SHOJI K.;
RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -1- FUNCTION: CHLOPOBLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANS. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PROSTHATIDYLGLYCEROL
CC

CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.

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CC

EMBL: U25817, G870784: -
CC

DR	PEPM; PF00487; FA-desaturase; 1.	CHLOROPLAST; MEMBRANE
KW	OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; TRANSIT PEPTIDE.	
KM		
FT	1	CHLOROPLAST (POTENTIAL).
CT	?	
CHARN	2	OMEGA-3 FATTY ACID DESATURASE
447		

	CONTAIN	1	47	CHLOROPLAST.	CHLOROPHYLL ACID DESATURASE
ET	DOMAIN	167	171	HISTIDINE BOX 1.	
ET	DOMAIN	203	271	HISTIDINE BOX 2.	
ET	DOMAIN	370	374	HISTIDINE BOX 3.	
CO	SEQUENCE	447-459	511-528	VAR. 670GGAGG CACCCTG	

SEQUENCE	44; AA;	3110 MM;	0/824/0B CIRC32;
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Matches	15; Conservative	0; Mismatches	0; Indels 0; Gaps 0

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Db      317 VMWLDVLTYLHHNGH 331
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Qy      112 VMWLDVLTYLHHNGH 126

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RESULT	3	
ID	FD31_BRANA	STANDARD;
		PRT;
		377 AA.

AC P46311;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)

DE (VERSION 1).
GN
FAD3.
OS
BRASSICA NAPUS (RAPE).
OC
EDUAROTIA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC
EDPHYLOPHYES: SEPTRAPANTOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEONS: ROSIDAE

```

OC CAPARALES; BRASSICACEAE; BRASSICA.
RN [1]
RP
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RX MEDLINE: 94302147.

```

RA YADAV N. S., WIERZBIICKI A., AEGERTER M., CASNER C. S., PEREZ-GRAU L.
RA KINNEY A. J., HITZ W. D., BOOTH J. R., JR., SCHWEIGER B., STECCA K. L.,
RA ALLEN S. M., BLACKWELL M., REITER R. S., CARLSON T. J., RUSSELL S. H.,
RA FELDMAN K. A., PIERCE J., BROWSE J.,
RA "Cloning of higher plant omega-3 fatty acid desaturases." *

RL PLANT PHYSIOL. 103:467-476(1993).

CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES

CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,

CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE

CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS

CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE

CC DOING AND PROVIDING FOR DOING PART CONTAIN THE POLY
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES
CC
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CC or send an email to license@slid.sld.cn)
--
DR EMBL; L22962; G408492; -
DR PFAM; pf00487; FA_desaturase_1.
KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM

KW	TRANSMEMBRANE.	
FT	TRANSMEM	54
FT	TRANSMEM	226
FT	TRANSMEM	203
FT	DOMAIN	92
		96
	POTENTIAL.	
	POTENTIAL.	
	POTENTIAL.	
	HISTIDINE BOX 1.	

Query Match	7.1%;	Score 9;	DB 1;	Length 377;
FT DOMAIN	128	132	HISTIDINE BOX 2.	
FT DOMAIN	295	299	HISTIDINE BOX 3.	
SO SEQUENCE	377 AA;	43258 MM;	247237E0 CRC32;	

	Best Local Similarity	100.0%;	Pred.	No. 5.59e-06;	
Matches	9;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
Db	248 VTJLHHGH	256	()		

QY	118	VTYLHHHGH	126
RESULT	4		
ID	FD3E SOYBN	STANDARD:	PRT: 380 AA

AC P48625: 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE. ENDOPLASMIC RETICULUM (EC 1.14.99.-)

GEN	GLYCINE MAX (SOYBEAN)
GN	FAD3.
OS	

OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-SEED;
 RA MEDLINE: 94302147.
 RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMAN K.A., PIERCE J., BROWSE J.,
 RT Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: MICROSOXAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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 CC -----
 DR EMBL: L22964; G408794; -
 DR PIR: JQ2338; JQ2338.
 DR PFAM: PF00487; FA_desaturase; 1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 55 75 POTENTIAL.
 FT TRANSMEM 212 232 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT DOMAIN 100 104 HISTIDINE BOX 1.
 FT DOMAIN 136 140 HISTIDINE BOX 2.
 FT DOMAIN 303 307 HISTIDINE BOX 3.
 SQ SEQUENCE 380 AA; 44185 MW; E3C509B7 CRC32;
 Query Match 7.1%; Score 9; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 5.59e-06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 256 VTYLHHGH 264
 QY 118 VTYLHHGH 126
 RESULT 5
 ID FD32.BRANA STANDARD; PRT; 383 AA.
 AC P48624;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (BC 1.14.99.-)
 DE (VERSION 2).
 GN PAD3
 OS BRASSICA NAPUS (RAPE).
 OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPRALES; BRASSICACEAE; BRASSICA.
 [1]
 RN SEQUENCE FROM N.A.
 RA MEDLINE: 93088059.
 RA ARONDEL V., LEMIEUX B., HWANG I., GIBSON S., GOODMAN H.M.,
 RA SOMERVILLE C.R.;

RT "Map-based cloning of a gene controlling omega-3 fatty acid
 RT desaturation in Arabidopsis.";
 RL SCIENCE 258:1353-1355(1992).
 CC -1- FUNCTION: ER (MICROSOXAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC -----
 DR EMBL: L01418; G167148; -
 DR PIR: PF00487; FA_desaturase; 1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 53 73 POTENTIAL.
 FT TRANSMEM 210 230 POTENTIAL.
 FT TRANSMEM 234 254 POTENTIAL.
 FT DOMAIN 98 102 HISTIDINE BOX 1.
 FT DOMAIN 134 138 HISTIDINE BOX 2.
 FT DOMAIN 301 305 HISTIDINE BOX 3.
 SQ SEQUENCE 383 AA; 43936 MW; F39A978B CRC32;
 Query Match 7.1%; Score 9; DB 1; Length 383;
 Best Local Similarity 100.0%; Pred. No. 5.59e-06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 254 VTYLHHGH 262
 QY 118 VTYLHHGH 126
 RESULT 6
 ID FD3E.ARAH STANDARD; PRT; 386 AA.
 AC P48623;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (BC 1.14.99.-).
 GN PAD3 OR F23F1.10.
 OS ARABIDOPSIS THALIANA (MOOSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPRALES; BRASSICACEAE; ARABIDOPSIS.
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA; TISSUE-SEEDLING;
 RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMAN K.A., PIERCE J., BROWSE J.,
 RT Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA; TISSUE-HYPOCOTYL;
 RA WATAHITI M.C., YAMAMOTO K.T.;
 RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
 [3]
 RN SEQUENCE FROM N.A.

RC STRAIN-CV, COLUMBIA;
RX MEDLINE; 94345020.
RA NISHIMURA T., NISHIMURA M., ARONDEL V., IBA K.;
RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
fatty acid desaturase from Arabidopsis thaliana.";
RL PLANT PHYSIOL. 105:767-768(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA;
RA ROUNTSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
RA SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
RA SOMERVILLE C.R., VENTER J.C.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -1- FUNCTION: MICROSOAM (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
CC DETECTABLE IN ROOT TISSUE.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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DR EMBL; L22931; G408483; -;
DR EMBL; D17579; G471091; -;
DR EMBL; D26508; G1197795; -;
DR EMBL; AC004680; G3420053; -;
DR PRAM; PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KM TRANSMEMBRANE.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 220 240 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
FT DOMAIN 101 105 HISTIDINE BOX 1.
FT DOMAIN 137 141 HISTIDINE BOX 2.
FT DOMAIN 304 308 HISTIDINE BOX 3.
SQ SEQUENCE 386 AA; 44076 MW; C2284B8C CRC32;

Query Match 7.1%; Score 9; DB 1; Length 386;
Best Local Similarity 100.0%; Pred. No. 5.59e-06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 257 VTYLHHGH 265
QY 118 VTYLHHGH 126

RESULT 7
ID FD3C.BRAN STANDARD; PRT; 404 AA.
AC P48618;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-)
DE (FRAGMENT).
GN FAD7.
OS BRASSICA NAPUS (RAPE).
OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPRALES; BRASSICACEAE; BRASSICA.
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE-SEED;
RX MEDLINE; 94302147.
RA YADAV N.S., WIRZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWIEGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMANN K.A., PIERCE J., BROWSE J.;
RL Cloning of higher plant omega-3 fatty acid desaturases.";
RT PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALCOPOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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DR EMBL; L22963; G408490; ALT_INIT.
DR PR: P00812; P00812.
DR PRAM; PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT NON_TER 1 1
FT TRANSIT <1 1
FT CHAIN ? 404
FT DOMAIN 121 125 CHLOROPLAST (POTENTIAL).
FT DOMAIN 157 161 OMEGA-3 FATTY ACID DESATURASE.
FT DOMAIN 324 328 HISTIDINE BOX 1.
FT DOMAIN 324 328 HISTIDINE BOX 2.
SQ SEQUENCE 404 AA; 46617 MW; 797F19FB CRC32;

Query Match 7.1%; Score 9; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 5.59e-06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 277 VTYLHHGH 285
QY 118 VTYLHHGH 126

RESULT 8
ID FD3D.ARA TH STANDARD; PRT; 435 AA.
AC P48622;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
DE PRECURSOR (EC 1.14.99.-).
GN FAD8.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPRALES; BRASSICACEAE; ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA; TISSUE=ARIAL PARTS;
RX MEDLINE; 95148742.
RA GIBSON S., ARONDEL V., IBA K., SOMERVILLE C.R.;
RT "Cloning of a temperature-regulated gene encoding a chloroplast
omega-3 desaturase from Arabidopsis thaliana.";
RL PLANT PHYSIOL. 106:1615-1621(1994).
RN [2]


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Db 390 LIAFPVYL 397
    |||||
QY 40 LIAFPVYL 47

RESULT 14
ID MPT_ECOLI STANDARD: PRT: 418 AA.
AC P77589; P77037;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE PUTATIVE 3-HYDROXYPHENYLPROPIONIC ACID TRANSPORTER.
GN MPT.
OS ESCHERICHIA COLI.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIAEAE;
OC ESCHERICHIA.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE: 97426617.
RA BLATTNER F.R., BLUKETT G. II, BLOCH C.A., PERNA N.T., BURLAND V.,
RA RILEY M., COLLADO-VIDES J., GLASER F.D., RODE C.K., MAYHEW G.F.,
RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
RA MAU B., SHAO Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL SCIENCE 277:1453-1474(1997).
RN [2]
RC SEQUENCE FROM N.A.
RA DUNCAN M., ALLEN E., ARAUJO R., APARICIO A.M., CHUNG E., DAVIS K.,
RA FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O., LEW H., LIN D.,
RA NAAATH A., OEFNER P., ROBERTS D., SCHRAMM S., DAVIS R.W.;
RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RC SEQUENCE FROM N.A.
RA STRAIN-K12;
RA MASHIMOTO H., SAITO N.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RC SEQUENCE OF CS525 FROM N.A.
RC STRAIN-K12 / CS520;
RA FERRANDEZ A., GARCIA J.L., DIAZ E.;
RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: COULD BE A TRANSPORTER FOR 3-PHENYLPROPIONATE
(CC (HYDROXYCINNAMIC ACID)).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
(CC (POTENTIAL)).
CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
CC FRAMESHIFTS.
CC -----
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CC -----
DR EMBL; AE000142; G1786549; -.
DR EMBL; U73857; G1657549; -.
DR EMBL; D85613; ?; NOT_ANNOTATED_CDS.
DR EMBL; X97543; E242997; -.
DR ECOGENE; EG13293; MPT.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
DR PFM; PF00083; sugar_tr; 1.
KW TRANSMEM; TRANSMEMBRANE; INNER MEMBRANE; SYMPORT.
FT TRANSMEM 32 52 POTENTIAL.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 97 117 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 158 178 POTENTIAL.

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FT  TRANSMEM  180  200  POTENTIAL.
FT  TRANSMEM  233  253  POTENTIAL.
FT  TRANSMEM  269  289  POTENTIAL.
FT  TRANSMEM  295  315  POTENTIAL.
FT  TRANSMEM  322  342  POTENTIAL.
FT  TRANSMEM  355  375  POTENTIAL.
FT  TRANSMEM  385  405  POTENTIAL.
FT  CONFLICT  310  310  L -> V (IN REF. 4).
SQ  SEQUENCE  418 AA; 43417 MW; AE3D1B8F CRC32;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 418;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db  305 MLASLLA 311
    |||||
QY  84 MLASLLA 90

RESULT  15
ID  PLO1_CHICK  STANDARD;  PRT;  730 AA.
AC  P24802;
DT  01-MAR-1992 (REL. 21, CREATED)
DT  01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT  15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE  PROCOLLAGEN-LYSINE/2-OXOGLUTARATE 1 PRECURSOR
    (EC 1.14.11.4) (LYSL HYDROXYLASE 1) (LH1).
GN  PLOD1 OR PLOD.
OS  GALUS GALLUS (CHICKEN).
OC  EUKARYOTA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC  NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
RN  [1]
RP  SEQUENCE FROM N.A., AND SEQUENCE OF 21-40; 412-417; 508-515 & 550-573.
RX  MEDLINE; 9131570.
RA  KIVIRIKKO K.I., TURPENNIEMI-HUJANEN T., PAJUNEN L.,
RA  PIHLAJANIEMI T., MYLLYLA R.;
RT  "Molecular cloning of chick lysyl hydroxylase. Little homology in
RT  primary structure to the two types of subunit of prolyl
RT  4-hydroxylase."
RL  J. BIOL. CHEM. 266:2805-2810(1991).
CC  -1- FUNCTION: FORMS HYDROXYLYSINE RESIDUES IN -XAA-LYS-GLY- SEQUENCES
CC  IN COLLAGENS. THESE HYDROXYLYSINES SERVE AS SITES OF ATTACHMENT
CC  FOR CARBOHYDRATE UNITS AND ARE ESSENTIAL FOR THE STABILITY OF THE
CC  INTERMOLECULAR COLLAGEN CROSSLINKS.
CC  -1- CATALYTIC ACTIVITY: PROCOLLAGEN L-LYSINE + 2-OXOGLUTARATE + O(2) =
CC  PROCOLLAGEN 5-HYDROXY-L-LYSINE + SUCCINATE + CO(2).
CC  -1- COFACTOR: REQUIRES IRON AND ASCORBATE.
CC  -1- SUBUNIT: HOMODIMER.
CC  -1- SUBCELLULAR LOCATION: MEMBRANE BOUND IN CISTERNAE OF ROUGH
CC  ENDOPLASMIC RETICULUM.
CC  -1- SIMILARITY: BELONGS TO THE LYSYL HYDROXYLASE FAMILY.
CC  -----
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CC  -----
DR  EMBL: M59183; G212282; -
DR  PIR: A23742; A23742; -
DR  PROSITE: PS01325; LYS_HYDROXYLASE; 1.
KW  OXIDOREDUCTASE; DIOXYGENASE; SIGNAL; IRON; VITAMIN C; GLYCOPROTEIN;
KW  ENDOPLASMIC RETICULUM; MEMBRANE.
FT  SIGNAL  1  20
FT  CHAIN  21  730  LYSYL HYDROXYLASE 1.
FT  METAL  659  659  IRON (BY SIMILARITY).
FT  METAL  661  661  IRON (BY SIMILARITY).
FT  METAL  711  711  IRON (BY SIMILARITY).
FT  ACT_SITE  721  721  POTENTIAL.
FT  CARBOHYD  200  200  POTENTIAL.
FT  CARBOHYD  403  403  POTENTIAL.

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FT  CARBOHYD  541  541  POTENTIAL.
FT  CARBOHYD  689  689  POTENTIAL.
SQ  SEQUENCE  730 AA; 84318 MW; B2A6C014 CRC32;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 730;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db  625 PITEKLY 631
    |||||
QY  16 PITEKLY 22

Search completed: Sat Aug 21 12:51:58 1999
Job time : 18 secs.

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Msearch_p protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:52:15 1999; Maspar time 9.96 Seconds
690.478 Million cell updates/sec

Tabular output not generated.

Title: >US-09-219-935-15
Description: (1-126) from US09219935.pep
Perfect Score: 126
Sequence: 1 HHQNHGTHRDESMHPIREK.....PVLVFMVMDLVLYLHHGH 126

Scoring table: TABLE uniprottable
Gap 60

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl9
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus

Statistics: Mean 3.195; Variance 0.413; scale 7.739

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	20	15.9	381 10	P94013	W-3 FATTY ACID DESATUR	4.43e-34
2	16	12.7	441 10	P93350	OMEGA-3 FATTY ACID DES	6.47e-23
3	15	11.9	383 10	065792	OMEGA-3 FATTY ACID DES	3.26e-20
4	13	10.3	438 10	004807	OMEGA-3 FATTY ACID DES	6.00e-15
5	10	7.9	350 2	007872	OMEGA-3 DESATURASE.	1.58e-07
6	9	7.1	380 10	023802	PLASTID OMEGA-3 FATTY	3.12e-05
7	9	7.1	398 10	024626	FATTY ACID DESATURASE	3.12e-05
8	9	7.1	407 10	064907	OMEGA-3 DESATURASE (FR	3.12e-05
9	9	7.1	431 10	082068	W-3 DESATURASE.	3.12e-05
10	9	7.1	438 10	P93452	OMEGA-3 FATTY ACID DES	3.12e-05
11	9	7.1	443 10	023824	FATTY ACID DESATURASE.	3.12e-05
12	7	5.6	254 1	027483	HYPOTHETICAL 28.3 KD P	4.90e-01
13	7	5.6	255 2	083255	COBALT ABC TRANSPORTER	4.90e-01
14	7	5.6	419 2	005589	HYPOTHETICAL 38.8 KD P	4.90e-01
15	7	5.6	436 10	040118	DELTA-15 LINOLEYL DESAT	4.90e-01
16	7	5.6	570 11	008700	RVP545	4.90e-01
17	7	5.6	570 11	P97390	VACUOLAR PROTEIN SORTI	4.90e-01
18	7	5.6	570 11	015715	VACUOLAR PROTEIN SORTI	4.90e-01
19	6	4.8	135 14	091954	POLYPROTEIN (FRAGMENT)	3.28e+01
20	6	4.8	157 4	Q15619	PUTATIVE OLFACTORY REC	3.28e+01

RESULT ID	AC	ID	PRELIMINARY;	PRT;	381 AA.
1	P94013				
2	P94013				
3	01-MAY-1997 (TREMBLREL. 03, CREATED)				
4	01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)				
5	01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)				
6	W-3 FATTY ACID DESATURASE.				
7	ORYZA SATIVA (RICE).				
8	OC EMBRYOTRANSFERRIN: STREPTOPHYTES; EMBRYOTRANSFERRIN: TRACHEOPHYTES;				
9	OC EUPHYLLIOTRANSFERRIN: SPERMATOPHYTES; MAGNOLIOPHYTES; LILIOPSIDA; POALES;				
10	OC POACEAE; ORYZA.				
11	RP SEQUENCE FROM N.A.				
12	RC STRAIN-IR36, AND NIPPONBARE;				
13	AKAGI H.;				
14	RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.				
15	DR EMBL; D78506; G17737376; -				
16	DR EMBL; D78505; G1785856; -				
17	DR MENDEL; 9612; Oryza; 1208; 1.				
18	SO SEQUENCE 381 AA; 43640 MW; 2BD4ED6E CRC32;				

Query Match 15.9%; Score 20; DB 10; Length 381;
Best Local Similarity 100.0%; Pred. No. 4.43e-34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB	241	PVLVFMVMDLVLYLHHGH 260
QY	107	PVLVFMVMDLVLYLHHGH 126

RESULT 2
AC P93350; PRELIMINARY; PRT; 441 AA.
ID P93350;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
GN NTFEAD7.
OS NICOTIANA TABACUM (COMMON TOBACCO).
OC EMBRYOTRANSFERRIN: STREPTOPHYTES; EMBRYOTRANSFERRIN: TRACHEOPHYTES;
OC EUPHYLLIOTRANSFERRIN: SPERMATOPHYTES; MAGNOLIOPHYTES; LILIOPSIDA; POALES;
OC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANALES; SOLANALES; SOLANALES; SOLANALES;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE; 96416425.
RA HANADA T., NISHIOCHI T., KODAMA H., NISHIMURA M., IBA K.;
RT "cDNA cloning of a wounding-inducible gene encoding a plastid omega-3
fatty acid desaturase from tobacco";
RL PLANT CELL PHYSIOL. 37:606-611(1996).
DR EMBL; D79979; D1012141; -.
DR PFAM; PF00487; FA_desaturase; 1.
DR MENDEL; 9312; NICTA;1208;2.
SQ SEQUENCE 441 AA; 50310 MW; 255F96A6 CRC32;

Query Match 12.7%; Score 16; DB 10; Length 441;
Best Local Similarity 100.0%; Pred. No. 6,47e-23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 311 FVWMDLVLYLHHGH 326
OY 111 FVWMDLVLYLHHGH 126
|||||

RESULT 3
ID 065792 PRELIMINARY; PRT; 383 AA.
AC 065792;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
GN TAFAD3.
OS TRITICUM AESTIVUM (WHEAT).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; TRITICUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, CHIHOKU; TISSUE-LEAF, AND ROOT;
RA HORIGUCHI G., KAKAKAMI N., KUSUMI K., KODAMA H., IBA K.;
RL PLANT CELL PHYSIOL. 39:540-544(1998).
DR EMBL; D84678; D1029298; -.
SQ SEQUENCE 383 AA; 43687 MW; 50D38F40 CRC32;

Query Match 11.9%; Score 15; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 3,26e-20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 248 VMMDLVLYLHHGH 262
OY 112 VMMDLVLYLHHGH 126
|||||

RESULT 4
ID 004807 PRELIMINARY; PRT; 438 AA.
AC 004807;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PERILLA FRUTESCENS.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANACEAE; LAMIALES; LAMIACEAE; PERILLA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OKDONG;
RA LEE S.K., KIM K.H., KIM Y.M., HWANG Y.S.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U59477; G1754795; -.
DR PFAM; PF00487; FA_desaturase; 1.
DR MENDEL; 16268; PERI;1208;mm16268.
SQ SEQUENCE 438 AA; 50160 MW; EE726819 CRC32;

Query Match 10.3%; Score 13; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 6,00e-15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 315 WLDLVLYLHHGH 327
OY 114 WLDLVLYLHHGH 126
|||||

RESULT 5
ID 007872 PRELIMINARY; PRT; 350 AA.
AC 007872;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE OMEGA-3 DESATURASE.
GN DESB.
OS SYNECHOCOCCUS PCC7002.
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97260123.
RA SAKAMOTO T., BRYANT D.A.;
RT "Temperature-regulated mRNA accumulation and stabilization for fatty
acid desaturase genes in the cyanobacterium Synechococcus sp. strain
PCC 7002";
RL MOL. MICROBIOL. 23:1281-1292(1997).
DR EMBL; U36389; G2197199; -.
DR PFAM; PF00487; FA_desaturase; 1.
SQ SEQUENCE 350 AA; 40562 MW; 969CAD61 CRC32;

Query Match 7.9%; Score 10; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1,58e-07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 238 WLDLVLYLHH 247
OY 114 WLDLVLYLHH 123
|||||

RESULT 6
ID 023802 PRELIMINARY; PRT; 380 AA.
AC 023802;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PLASTID OMEGA-3 FATTY ACID DESATURASE (FRAGMENT).
GN TAFAD7.
OS TRITICUM AESTIVUM (WHEAT).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; TRITICUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, CHIHOKU; TISSUE-LEAF;
RA HORIGUCHI G., IYAKAWA H., KODAMA H., KAKAKAMI N., NISHIMURA M.,
RA IBA K.;
RL PHYSIOL. PLANTARUM 96:275-283(1996).
DR EMBL; D43688; D1008371; -.
DR PFAM; PF00487; FA_desaturase; 1.
FT NON TER 1
SQ SEQUENCE 380 AA; 42633 MW; 2123FF56 CRC32;

Query Match 7.1%; Score 9; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 3,12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 255 VTYLHHGH 263
OY 118 VTYLHHGH 126
|||||

RESULT 7
ID 024626 PRELIMINARY; PRT; 398 AA.
AC 024626;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
GN FAD8.
OS ZEA MAYS (MAIZE).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-HONEY BANTUM AND HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
DR EMBL: D84409; D1023307; -;
DR EMBL: D63953; D1023305; -;
DR PFAM: PF00487; FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 398 AA; 44789 MW; 70565SEC CRC32;

Query Match 7.1%; Score 9; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 3.12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 272 VTYLHHGH 280
QY 118 VTYLHHGH 126
|||||

RESULT 8
ID 064907 PRELIMINARY; PRT; 407 AA.
AC 064907;
DT 01-AUG-1998 (TREMBREL. 07, CREATED)
DT 01-AUG-1998 (TREMBREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)
DE OMEGA-3 DESATURASE (FRAGMENT).
GN PXH-15.
OS PELARGONIUM X HORTORUM.
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC GERANIACEAE; PELARGONIACEAE; PELARGONIUM.
RN (1)
RP SEQUENCE FROM N.A.
RA SCHULTZ D.J., MUMMA R.O., COX-FOSTER D., CRAIG R., MEDFORD J.I.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF020204; G3133289; -;
FT NON_TER 1
SQ SEQUENCE 407 AA; 47169 MW; BC150974 CRC32;

Query Match 7.1%; Score 9; DB 10; Length 407;
Best Local Similarity 100.0%; Pred. No. 3.12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 279 VTYLHHGH 287
QY 118 VTYLHHGH 126
|||||

RESULT 9
ID 082068 PRELIMINARY; PRT; 431 AA.
AC 082068;
DT 01-NOV-1998 (TREMBREL. 08, CREATED)
DT 01-NOV-1998 (TREMBREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE W-3 DESATURASE.
OS SOLANUM TUBEROSUM (POTATO).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANACEAE; SOLANACEAE; SOLANUM.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RA LEON J.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RA MARTIN M.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: A0007739; E1318202; -;
SQ SEQUENCE 431 AA; 49253 MW; BAF99CD CRC32;

Query Match 7.1%; Score 9; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 308 VTYLHHGH 316
QY 118 VTYLHHGH 126
|||||

RESULT 10
ID P93452 PRELIMINARY; PRT; 438 AA.
AC P93452;
DT 01-MAY-1997 (TREMBREL. 03, CREATED)
DT 01-MAY-1997 (TREMBREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PETROSELINUM CRISPUM (PARSLEY) (PETROSELINUM HORTENSE).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; ARALIALES; APIACEAE; PETROSELINUM.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 97203190.
RA KIRSCH C., TAKAMIYA-WIK M., REINOLD S., HAHLEBROCK K., SOMSSICH I.E.;
RT "Rapid, transient, and highly localized induction of plastidial
RT omega-3 fatty acid desaturase mRNA at fungal infection sites in
RT Petroselinum crispum."
RL PROC. NATL. ACAD. SCI. U.S.A. 94:2079-2084(1997).
DR EMBL: U75745; G1786066; -;
DR PFAM: PF00487; FA_desaturase; 1.
DR MENDEL: 9788; Petcr; 1208.1
SQ SEQUENCE 438 AA; 50391 MW; 9E77A228 CRC32;

Query Match 7.1%; Score 9; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 3.12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 315 VTYLHHGH 323
QY 118 VTYLHHGH 126
|||||

RESULT 11
ID 023824 PRELIMINARY; PRT; 443 AA.
AC 023824;
DT 01-JAN-1998 (TREMBREL. 05, CREATED)
DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE.
GN FAD7.
OS ZEA MAYS (MAIZE).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
RN [2]
RP SEQUENCE OF 182-443 FROM N.A.
RC STRAIN-HONEY BANTUM;
RX MEDLINE: 98145435.
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RT "Two maize genes encoding omega-3 fatty acid desaturase and their
RT differential expression to temperature."
RN [2]

RL PLANT MOL. BIOL. 36:297-306(1998).
DR EMBL: D63954; D1023306; -.
DR EMBL: D63952; D1023304; -.
DR PFM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 443 AA; 49437 MW; E8BC6757 CRC32;

Query Match 7.1%; Score 9; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 3.12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 317 VTYLHHGH 325
|||||
QY 118 VTYLHHGH 126

RESULT 12
ID 027483 PRELIMINARY; PRT; 254 AA.
AC 027483;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HYPOTHEICAL 28.3 KD PROTEIN.
GN MTH1434.
OS METHANOBACTERIUM THERMAUTOTROPHICUM.
OC ARCHAEA; EURYARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAE;
OC METHANOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H:
RX MEDLINE: 98037514.
RA SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
RA ALDREGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
RA HARRISON D., HOANG L., KENGLE P., LUMM W., POTIER B., QIU D.,
RA SPADAFORA R., VICARIE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
RA JIWANI N., CARUSO A., BUSH D., SAFER R., PATMILL D., PRABHAKAR S.,
RA MCDONALD L., SHIMER G., GOVAL A., PIETROVSKI S., CHURCH G.M.,
RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REVEY J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT delah: functional analysis and comparative genomics.";
RL J. BACTERIOL. 179:7135-7155(1997).
DR EMBL: AE000905; G2622546; -.
KW HYPOTHEICAL PROTEIN.
SQ SEQUENCE 254 AA; 28253 MW; AA8DF6C5 CRC32;

Query Match 5.6%; Score 7; DB 1; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.90e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 220 YGIPYLV 226
|||||
QY 104 YGIPYLV 110

RESULT 13
ID 083255 PRELIMINARY; PRT; 255 AA.
AC 083255;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE COBALT ABC TRANSPORTER, ATP-BINDING PROTEIN.
GN T70227.
OS TREPONEMA PALLIDUM.
OC BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; TREPONEMA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98332770.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODDSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;

RT "Complete Genome Sequence of Treponema pallidum, the Syphilis
RT Spirochete.";
RL SCIENCE 281:375-388(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODDSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AE001204; G3322495; -.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-BINDING; TRANSPORT.
SQ SEQUENCE 255 AA; 27321 MW; 81400AE7 CRC32;

Query Match 5.6%; Score 7; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.90e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 104 CARGPLQ 110
|||||
QY 93 CARGPLQ 99

RESULT 14
ID 005589 PRELIMINARY; PRT; 419 AA.
AC 005589;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHEICAL 38.8 KD PROTEIN.
GN FV1004C.
OS MYCOBACTERIUM TUBERCULOSIS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; CORNEBACTERIINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE: 98295987.
RA COLE S.T., BROSCHE R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.,
RA GORDON S.V., EIGLMEIER K., GAS S., BARRY III C.E., TEKAIA F.,
RA BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
RA DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S.,
RA HORNSEY T., JAGELS K., KROGH A., MCLEAN J., MOUE S., MURPHY L.,
RA OLIVER S., OSBORNE J., O'GAIL M.A., RAJANDREAN M.A., ROGERS J.,
RA RUTTER S., SEEGER K., SKELTON S., SQUARES S., SOARES R., SULSTON J.E.,
RA TAYLOR K., WHITEHEAD S., BARRELL B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL NATURE 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX PARKHILL J.;
RL SUBMITTED (JUN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Z94752; E1299781; -.
KW HYPOTHEICAL PROTEIN.
SQ SEQUENCE 419 AA; 38785 MW; 4B1AD82D CRC32;

Query Match 5.6%; Score 7; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 4.90e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 254 ASLAMA 260
|||||
QY 86 ASLAMA 92

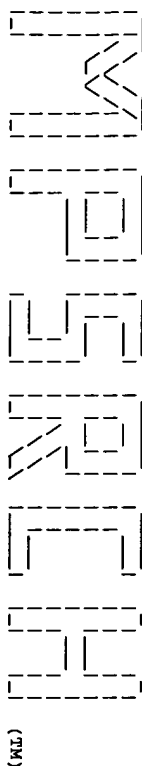
RESULT 15
ID Q40118 PRELIMINARY; PRT; 436 AA.

AC 040118;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE DELTA-15 LINEOYL DESATURASE.
 OS LIMNANTHES DOUGLASSII.
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTES; EMBRYOPHYTES; TRACHEOPHYTES;
 OC EUPHYLOPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTES; EUDICOTYLEDONS; ROSIDAE;
 OC CAPRIFOLIACEAE; LIMNANTHACEAE; LIMNANTHES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95334518.
 RA BHELIA R.S.; MACKENZIE S.L.;
 RT "Nucleotide sequence of a cDNA from Limnantes douglasii L. encoding
 a delta-15 linoleic acid desaturase.";
 RL PLANT PHYSIOL. 108:861-861(1995).
 DR EMBL; U17063; G699390; -.
 DR FRAM; PF00487; FA_desaturase; 1.
 DR MENDEL; 8699; LINDO; 1208; 1.
 SQ SEQUENCE 436 AA; 50093 MW; 327D77FE CRC32;

Query Match 5.6%; Score 7; DB 10; Length 436;
 Best Local Similarity 100.0%; Pred. No. 4.90e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 194 HHONHGH 200
 QY 1 HHONHGH 7

Search completed: Sat Aug 21 12:52:57 1999
 Job time : 42 secs.

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(TM)

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Search: protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:49:24 1999; Maspar time 6.93 Seconds

Tabular output not generated. 386,472 Million cell updates/sec

Title: >US-09-219-935-15

Description: (1-126) from US09219935.pep

Perfect Score: 126

Sequence: 1 HHQNHGTHRDESMHPIREK.....PVLVFMVMDLVYTLHHGH 126

Scoring table: TABLE uniprottable

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

a:geneseqs

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 2.519; Variance 0.623; scale 4.044

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	126	100.0	126	7	Sequence of an intern	1.21e-197
2	16	12.7	453	7	Sequence of soybean p	1.24e-12
3	10	7.9	447	24	Sesame omega-3 alipha	6.26e-04
4	9	7.1	378	7	Sequence of microsoma	1.40e-02
5	9	7.1	380	7	Sequence of microsoma	1.40e-02
6	9	7.1	383	11	Linoleic-acid-desatur	1.40e-02
7	9	7.1	386	7	Sequence of delta-15	1.40e-02
8	9	7.1	387	7	Sequence of delta-15	1.40e-02
9	9	7.1	404	7	Sequence of plastid d	1.40e-02
10	9	7.1	435	11	Linoleic-acid-desatur	1.40e-02
11	9	7.1	446	11	Linoleic-acid-desatur	1.40e-02
12	9	7.1	446	7	Sequence of a plastid	1.40e-02
13	7	5.6	156	7	Sequence of a plastid	4.96e+00
14	6	4.8	447	2	Sequence of flagellin	4.96e+00
15	6	4.8	68	29	H. pylori ORF hp4p113	7.37e+01
16	6	4.8	131	22	H. pylori putative tr	7.37e+01
			160	5	Pheromone receptor cl	7.37e+01
					R27885	

17	6	4.8	168	21	W20521	Helicobacter pylori c	7.37e+01
18	6	4.8	170	29	W44794	B. afzelii strain B02	7.37e+01
19	6	4.8	197	31	W59156	H. influenza rhnb pro	7.37e+01
20	6	4.8	260	28	W36115	Yeast ribosomal prote	7.37e+01
21	6	4.8	301	22	W20732	H. pylori cell envelo	7.37e+01
22	6	4.8	318	25	W32065	Human beta-sarcoglyca	7.37e+01
23	6	4.8	318	25	W32064	Human beta-sarcoglyca	7.37e+01
24	6	4.8	318	25	W32060	H. sapiens beta-sarco	7.37e+01
25	6	4.8	318	25	W32066	Human beta-sarcoglyca	7.37e+01
26	6	4.8	322	25	R26065	Encodes rat CRP-bindi	7.37e+01
27	6	4.8	322	29	W52177	Human CRP-binding pro	7.37e+01
28	6	4.8	322	29	W52178	Rat CRP-binding prote	7.37e+01
29	6	4.8	324	20	W11860	Human proteosome subu	7.37e+01
30	6	4.8	324	13	R74000	Full length ovine CRF	7.37e+01
31	6	4.8	342	26	W26671	Mouse alpha-fucosyltr	7.37e+01
32	6	4.8	342	21	W11820	Murine myeloid-linag	7.37e+01
33	6	4.8	356	26	W26676	Borrelia variabile maj	7.37e+01
34	6	4.8	361	18	R20816	Human epithelial CD44	7.37e+01
35	6	4.8	361	18	R91444	Human haematopoietic	7.37e+01
36	6	4.8	362	1	R07355	B7 adhesion receptor.	7.37e+01
37	6	4.8	454	18	R97842	Kaposi's sarcoma asso	7.37e+01
38	6	4.8	454	17	R93616	Kaposi's sarcoma asso	7.37e+01
39	6	4.8	453	17	R91445	Human epithelial CD44	7.37e+01
40	6	4.8	493	4	R20817	Human epithelial CD44	7.37e+01
41	6	4.8	653	7	R37425	Epithelial CD44 Antis	7.37e+01
42	6	4.8	680	2	R07453	IDUA.	7.37e+01
43	6	4.8	680	30	R07456	First open reading fr	7.37e+01
44	6	4.8	719	38	W82644	Saccharomyces cerevis	7.37e+01
45	6	4.8	1275	39	W82594	Enfilonia sp. extende	7.37e+01
						H. contortus PGP-A pr	7.37e+01

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	Description
1	R37597	100.0%	Score 126;	DB 7;	Length 126;
AC	R37597				
DT	01-OCT-1993 (first entry)				
DE	Sequence of an internal region of a corn seed delta-15				
DE	desaturase.				
KW	Lipid composition; modification; fatty acid desaturase; enzyme.				
OS	Zea mays, clone pPCR20.				
PN	W09311245-A.				
PD	10-JUN-1993.				
PF	03-DEC-1992; U10284.				
PR	04-DEC-1991; US-804259.				
PA	(DUPD) DU PONT DE NEMOURS & CO E. I.				
PI	Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, Yadvav NS;				
DR	WPI: 93-197063/24.				
DR	N-PDB: Q43209.				
PT	Isolated nucleic acid fragment, for plant lipid compsn.				
PT	acid desaturase or related enzyme with high aminoacid identity to				
PT	specific polypeptide				
PS	disclosure: Page 152-153; 167pp; English.				
CC	PCR3 was isolated from a cDNA library using a 5.2 kb Hind III				
CC	fragment containing wild-type genomic DNA as a radiolabeled				
CC	hybridization probe. One of the sequencing primers made to the PCR3				
CC	insert was also used. The identity of the expression product of PCR3				
CC	as the Arabidopsis microsomal delta-15 desaturase was confirmed by				
CC	its biological overexpression in plant tissues. Conserved regions of				
CC	R37592 are useful in designing long oligomers for hybridization as				
CC	well as shorter ones for use as primers in the PCR. The sequences				
CC	of useful regions are given in Q43213-Q43224. Q43209 is the				
CC	complete nucleotide sequence of a 396 bp polymerase chain reaction				
CC	product derived from corn seed mRNA that is found in the insert of				
CC	plasmid pPCR20. Nucleotides 1 to 31 and 364 to 396 correspond to				
CC	the amplification primers described in Q43221 and Q43222				
CC	respectively. Nucleotides 31 to 363 encode a region that is 61.98				
CC	identical to the region between amino acids 137 and 249 of R37591.				
SQ	Sequence 126 AA;				

```

Dd      1 hnhghthhdaeswhpleklyrgleprtklktftvfpfllaipvylltyspgklqshfl 60
        |||||||
Qy      1 HNHGHHHRDSNHPHTEKLYRDLERPTKKLRRTYVFPPLAFAYVLLYSFGKLSHFL 60
        |||||||

Dd      61 psadfspeksdvmsvtcwcmlasllamacafgplqvlkmgyldylyfvwmldvty 120
        |||||||
Qy      61 PSSDFSPKESDVMSVTTCWCIMLASLAWACAFGLQVLKMGIPLYLVFWMLDVLT 120
        |||||||

Dd      121 lhhgh 126
        |||||||
Qy      121 LHHGH 126

RESULT      2
ID          R37596 standard; Protein; 453 AA.
AC          R37596;
DC          01-OCT-1993 (first entry)
DE          Sequence of soybean plastid delta-15 desaturase.
KW          Lipid composition; modification; fatty acid desaturase; enzyme.
OS          Glycine max, clone pSFD-118bpw.
PN          M093J1245-A.
PE          10-JUN-1993.
PF          03-DEC-1992; U10284.
PR          04-DEC-1991; US-804259.
PA          (DUPLO ) DU POINT DE NEMOURS & CO E.I.
PI          Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI          Yadav NS, Wepi: 93-197063/24.
DR          N-PSSB; Q43208.
PT          Isolated nucleic acid fragment, for plant lipid compsn.
PT          modification - comprises nucleic acid sequence encoding fatty
PT          acid desaturase or related enzyme with high aminoacid identity to
PT          specific polypeptide.
PS          Disclosure; Page 148-150; 167Pp; English.
PC          PCR3 was isolated from a cDNA library using a 5.2 kb Hind III
CC          fragment containing wild-type genomic DNA as a radiolabeled
CC          hybridization probe. One of the sequencing primers made to the PCR3
CC          insert was also used. The identity of the expression product of PCR3
CC          as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC          its biological overexpression in plant tissues. Conserved regions of
CC          R37592 are useful in designing long oligomers for hybridization as
CC          well as shorter ones for use as primers in the PCR. The sequences
CC          of useful regions are given in Q43213-Q43224. Arabidopsis delta-15
CC          desaturase cDNA was used as a hybridization probe to isolate a
CC          glycerolipid desaturase cDNA from soybean. Plasmid pXf1 was
CC          deposited under ATCC 68874. Soybean microsomal delta-15
CC          desaturase cDNA was used as a hybridization probe to isolate cDNAs
CC          encoding related desaturases from soybean. The insert of
CC          pSFD-118bpw contained a stretch of 1675 nucleotides which contained
CC          an open-reading frame encoding a polypeptide (R37596) of about
CC          806 identity with, and colinear with, the Arabidopsis plastid
CC          delta-15 desaturase polypeptide listed in R37593. Nucleotides 169
CC          to 382 encode the putative plastid transit peptide, colinear with
CC          CC and sharing some homology with the transit peptide described for
CC          the Arabidopsis plastid delta-15 glycerolipid desaturase (R37593).
SQ          Sequence 453 AA;

Query Match      12.7%; Score 16; DB 7; Length 453;
Best Local Similarity 100.0%; Pred.No. 1,24e-12;
Matches      16; Conservative      0; Mismatches 0; Indels 0; Gaps 0;

Dd      320 fvmmldvtylhhgh 335
        |||||||
Qy      111 FVMMLDVTYLHHGH 126

RESULT      3
ID          W13381 standard; Protein; 447 AA.
AC          W13381;
DC          02-DEC-1997 (first entry)

```

DE	Sesame omega-3 aliphatic acid desaturase.
KW	sesame; omega-3 aliphatic acid desaturase; modify; fat; oil; plant;
RV	linoleic acid; recombinant production.
OS	Sesamum indicum.
PN	J09065882-A.
PD	11-MAR-1997.
PF	01-SEP-1995; 225145.
PR	01-SEP-1995; JP-225145.
PA	(TOYA-) TOYAMA KEN.
DR	WPI: 97-220417/20.
N-PSDB:	T62066.
PT	Sesame omega-3 aliphatic acid desaturase gene - useful in genetic engineering to modify fats and oils in agricultural products
PS	Claim 6; Page 4; 10pp; Japanese.
CC	This protein is a sesame omega-3 aliphatic acid desaturase. Its coding sequence can be used in genetic engineering to modify fats and oils in agricultural products. The gene or enzyme can be introduced into a plant to modify the aliphatic acid composition in its oils and fats, to give oils and fats with a high content of linolenic acid. Antisense DNA can be introduced into a plant to inhibit the expression of the gene, so that oils and fats with little or no linolenic acid are produced. The gene can also be expressed in microorganisms for recombinant production the enzyme.
SO	Sequence 447 AA;
Query Match	7.9%; Score 10; DB 24; Length 447;
Best Local Similarity	100.0%; Pred. No. 6,26e-04;
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dd	322 lvtvlyhhgh 331 QY 117 LVTYLHHGH 126
RESULT 4	
ID	R37591 standard; Protein; 378 AA.
AC	R37591;
DT	01-OCT-1993 (first entry)
DE	Sequence of microsomal delta-15 glycerolipid desaturase.
KW	Lipid composition; modification; fatty acid desaturase; enzyme.
RV	Brassica napus, clone PBNSF3-f2.
FN	W09311245-A.
PD	10-JUN-1993.
PF	03-DEC-1992; U10284.
PR	04-DEC-1991; US-804259.
PA	(DUPO.) DU PONT DE NEMOURS & CO E.I.
EI	Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
F1	Yaav NS;
DR	WPI: 93-197063/24.
N-PSDB:	Q43205.
PT	Isolated nucleic acid fragment, for plant lipid compsn.
PT	modification - comprises nucleic acid sequence encoding fatty acid desaturase or related enzyme with high aminoacid identity to specific polypeptide
PC	Disclosure; Page 136-138; 167pp; English.
PS	PCR3 was isolated from a cDNA library using a 5.2 kb Hind III fragment containing wild-type genomic DNA as a radiolabeled hybridization probe. One of the sequencing primers made to the PCR3 insert was also used. The identity of the expression product of PCR3 as the Arabidopsis microsomal delta-15 desaturase was confirmed by its biological overexpression in plant tissues. Conserved regions of R37592 are useful in designing long oligomers for hybridization as well as shorter ones for use as primers in the PCR. The sequences of useful regions are given in Q43213-Q43224. The cDNA inserts from PCR3 and PCR2 were used to isolate PBNSF3-2. Plasmid PBNSF3-2 was deposited at ATCC No. 68854. PBNSF4-3 (Q43206) corresp. to a novel Brassica napus seed desaturase different from that shown in Q43205.
SO	Sequence 378 AA;
Query Match	7.1%; Score 9; DB 7; Length 378;
Best Local Similarity	100.0%; Pred. No. 1,40e-02;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 251 vtylhhgh 259
 |||||||
 QY 118 VTYLHHGH 126

RESULT 5
 ID R37595 standard; Protein; 380 AA.

AC R37595;

DT 01-OCT-1993 (first entry)

DE Sequence of microsomal delta-15 desaturase.

KW Lipid composition; modification; fatty acid desaturase; enzyme.

OS Glycine max, clone pXf1.

PN MO9311245-A.

PD 10-JUN-1993.

PF 03-DEC-1992: U10284.

PI 04-DEC-1991: US-804259.

PA (DUPO) DU PONT DE NEMOURS & CO E. I.

PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, Yadvav NS;

DR WPI: 93-197063/24.

PT Isolated nucleic acid fragment, for plant lipid compsn.

PT acid desaturase or related enzyme with high aminoacid identity to

PT specific polypeptide

PS Disclosure: Page 144-146: 167pp; English.

CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III

CC fragment containing wild-type genomic DNA as a radiolabeled

CC hybridization probe. One of the sequencing primers made to the PCF3

CC insert was also used. The identity of the expression product of PCF3

CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by

CC its biological overexpression in plant tissues. Conserved regions of

CC R37592 are useful in designing long oligomers for hybridization as

CC well as shorter ones for use as primers in the PCR. The sequences

CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15

CC desaturase cDNA was used as a hybridization probe to isolate a

CC glycerolipid desaturase cDNA from soybean. Plasmid pXf1 was

CC deposited under ATCC 68874.

CC Sequence 380 AA;

SO

Query Match

Best Local Similarity 100.0%; Pred. No. 1.40e-02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 256 vtylhhgh 264

|||||||

QY 118 VTYLHHGH 126

RESULT 6

ID R60498 standard; Protein; 383 AA.

AC R60498;

DT 28-MAR-1995 (first entry)

DE Linoletic-acid-desaturase: fad3.

KW Linoletic-acid-desaturase: fad3; oilseed rape; rapeseed;

KM transgenic plant; crop improvement; yeast artificial chromosome;

KW YAC; linoletic acid.

OS Brassica napus.

PN MO9418337-A.

PD 18-AUG-1994.

PF 04-FEB-1994: U01321.

PR 05-FEB-1993: US-014431.

PR 22-NOV-1993: US-156551.

PA (MONS) MONSANTO CO.

PA (UNMS) UNIV MICHIGAN STATE.

PI Aronoff VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR;

DR N-PSDB: 071203.

PT Genetically transformed plants with altered linoletic acid

PT content - contg recombinant, double-stranded DNA encoding

PT linoletic acid desaturase, or the antisense of the coding

PS Disclosure; Page 69-71; 144pp; English.
 CC cDNA encoding the linoletic-acid-desaturase (fad3) of B. napus was
 CC isolated from a YAC library using RFLP 220 and ASA2 markers as
 CC probes. Isolated DNA was amplified using the primers given in
 CC Q71204-09, and used to screen YAC libraries. The fad3 gene was
 CC identified in YAC EW/D11.
 SQ Sequence 383 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.40e-02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 254 vtylhhgh 262

|||||||

QY 118 VTYLHHGH 126

RESULT 7

ID R37592 standard; Protein; 386 AA.

AC R37592;

DT 01-OCT-1993 (first entry)

DE Sequence of delta-15 desaturase.

KW Lipid composition; modification; fatty acid desaturase; enzyme.

OS Arabidopsis thaliana, clone PCF3.

PN MO9311245-A.

PD 10-JUN-1993.

PF 03-DEC-1992: U10284.

PI 04-DEC-1991: US-804259.

PA (DUPO) DU PONT DE NEMOURS & CO E. I.

PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, Yadvav NS;

DR WPI: 93-197063/24.

PT Isolated nucleic acid fragment, for plant lipid compsn.

PT acid desaturase or related enzyme with high aminoacid identity to

PT specific polypeptide

PS Disclosure: Page 127-129: 167pp; English.

CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III

CC fragment containing wild-type genomic DNA as a radiolabeled

CC hybridization probe. One of the sequencing primers made to the PCF3

CC insert was also used. The identity of the expression product of PCF3

CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by

CC its biological overexpression in plant tissues. Conserved regions of

CC R37592 are useful in designing long oligomers for hybridization as

CC well as shorter ones for use as primers in the PCR. The sequences

CC of useful regions are given in Q43213-Q43224.

CC Sequence 386 AA;

SO

Query Match

Best Local Similarity 100.0%; Pred. No. 1.40e-02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 257 vtylhhgh 265

|||||||

QY 118 VTYLHHGH 126

RESULT 8

ID R37594 standard; Protein; 404 AA.

AC R37594;

DT 01-OCT-1993 (first entry)

DE Sequence of plastid delta-15 glycerolipid desaturase.

KW Lipid composition; modification; fatty acid desaturase; enzyme.

OS Brassica napus, clone pBNSfd-2.

PN MO9311245-A.

PD 10-JUN-1993.

PF 03-DEC-1992: U10284.

PI 04-DEC-1991: US-804259.

PA (DUPO) DU PONT DE NEMOURS & CO E. I.

PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, Yadvav NS;

DR WPI: 93-197063/24.

DR N-PSDB: 043206.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 140-141; 167pp; English.
CC PCR3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCR3
CC insert was also used. The identity of the expression product of PCR3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in 043213-043224. The cDNA inserts
CC from PCR3 and PCM2 were used to isolate PBNSF3-2. Plasmid PBNSF3-2
CC was deposited as ATCC No. 68854. PBNSF3-2 (043206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC 043205.
SQ Sequence 404 AA;

Query Match 7.1%; Score 9; DB 7; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.40e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 277 vtylhhgh 285
|||
OY 118 VTYLHHGH 126

RESULT 9
ID R60500 standard; Protein; 435 AA.
AC R60500; 28-MAR-1995 (first entry)
DE Linoleic-acid-desaturase fadD.
KW Linoleic-acid-desaturase; fadD; transgenic plant; crop improvement;
OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PA (UMMS) UNIV MICHIGAN STATE.
PI Arondei VJA, Gibson ST, Kishore GM, Ruff TG, Somerville CR;
DR WPI: 94-279758/34.
DR N-PSDB: 071211.
PT Genetically transformed plants with altered linolenic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoleic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure: Page 79-81; 144pp; English.
CC The cDNA sequence and deduced amino acid sequence of linoleic-
CC acid-desaturase fadD of Arabidopsis are provided.
SQ Sequence 435 AA;

Query Match 7.1%; Score 9; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.40e-02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 312 vtylhhgh 320
|||
OY 118 VTYLHHGH 126

RESULT 10
ID R60499 standard; Protein; 446 AA.
AC R60499; 28-MAR-1995 (first entry)
DE Linoleic-acid-desaturase fadD.
KW Linoleic-acid-desaturase; fadD; transgenic plant; crop improvement;
KW linolenic acid.

OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PA (UMMS) UNIV MICHIGAN STATE.
PI Arondei VJA, Gibson ST, Kishore GM, Ruff TG, Somerville CR;
DR WPI: 94-279758/34.
DR N-PSDB: 071210.
PT Genetically transformed plants with altered linolenic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoleic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure: Page 75-77; 144pp; English.
CC The cDNA sequence and deduced amino acid sequence of linoleic-
CC acid-desaturase fadD of Arabidopsis are provided.
SQ Sequence 446 AA;

Query Match 7.1%; Score 9; DB 7; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.40e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 319 vtylhhgh 327
|||
OY 118 VTYLHHGH 126

RESULT 11
ID R37593 standard; Protein; 446 AA.
AC R37593;
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone PACR2-2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: 043204.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 132-134; 167pp; English.
CC PCR3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the
CC insert was also used. The identity of the expression product of PCR3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in 043213-043224. In contrast to the
CC constitutive expression of the gene encoding (R37592), the mRNA
CC corresponding to 043204 is abundant in green tissues, rare in roots
CC and leaves, and is about three-fold more abundant in leaf than that
CC of 043202. R37592 and R37593 show overall homology of approx.
CC 80%.
SQ Sequence 446 AA;

Query Match 7.1%; Score 9; DB 7; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.40e-02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 319 vtylhhgh 327
|||
OY 118 VTYLHHGH 126

RESULT 12
ID R37598 standard; Protein: 156 AA.
AC R37598:
DT 01-OCT-1993 (first entry)
DE Sequence of a plasmid delta-15 fatty acid.
KW Lipid composition: modification: fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone pFedx-2 and pYacp7.
PN WO9311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PI (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, Yadau NS;
DR WPI: 93-197063/24.
DR N-PSDB: 043210.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PR modification - comprises nucleic acid sequence encoding fatty acid desaturase or related enzyme with high aminoacid identity to specific polypeptide
PS Disclosure: Page 155; 16pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III fragment containing wild-type genomic DNA as a radiolabeled hybridization probe. One of the sequencing primers made to the PCF3 insert was also used. The identity of the expression product of PCF3 as the Arabidopsis microsomal delta-15 desaturase was confirmed by its biological overexpression in plant tissues. Conserved regions of R37592 are useful in designing long oligomers for hybridization as well as shorter ones for use as primers in the PCR. The sequences of useful regions are given in 043213-043224. 043210 is the partial composite sequence derived from the inserts in plasmids pFedx-2 and pYacp7. R37598 is a deduced partial peptide sequence of its ORF.
SQ Sequence 156 AA:

Query Match 5.6%; Score 7; DB 7; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.96e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 147 hghnqh 153
| | | | | | | | | |
OY 1 HHQNHGH 7

RESULT 13
ID P70314 standard; Protein: 447 AA.
AC P70314:
DT 06-JUN-1991 (first entry)
DE Sequence of flagellin deletion mutant encoded by Escherichia coli
DE K-12 KH552 has gene in pFDJ3.
KW Secretion vector; secretion system: flagella.
OS Escherichia coli.
PN EP-237045-A.
PD 16-SEP-1987.
PF 11-MAR-1987; 103488.
PR 11-MAR-1986; JP-054400.
PR 19-SEP-1986; JP-223484.
PA (SHO) SHIONOGI & CO LTD.
PI Asaka J, Fujiwara T, Fujiwara T, Kuwajima G, Kondo E, Shin M;
DR WPI: 87-258329/37.
DR N-PSDB: N70503.
PT DNA encoding flagellin - used for fusing to foreign DNA for excretion of peptide(s), determ. of epitope(s) and prepn. of antigens
PT Example: Fig 15b; 119pp; English.
CC The hag gene encoding flagellin is inserted into a vector and then the hag gene is cut or partially deleted and linker DNA inserted.
CC DNA coding for a foreign peptide is inserted into the linker DNA and the vector introduced into a bacterium. As a result, the foreign peptide is excreted from the bacterium as a peptide is fused with flagellin. Under certain conditions the excreted peptide forms

CC flagella, thus facilitating the recovery of the peptide. The examples
CC prepare vectors contg. the hag gene (N70495) from which the sequence
CC between bp 583 to 1143 has been deleted (see N70496, N70497, N70500,
CC N70501, N70502, N70503, N70504).
SQ Sequence 447 AA:

Query Match 5.6%; Score 7; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 4.96e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 245 yrspgkl 251
| | | | | | | | | |
OY 49 YRSPGKL 55

RESULT 14
ID W55401 standard; Protein: 68 AA.
AC W55401:
DT 18-JUN-1998 (first entry)
DE H. pylori ORF hp4p1352orf5 protein.
KW Cytoplasmic; vaccine; prevention; treatment; infection; envelope;
KW Identification; binding compound; bacteria; life cycle; activator;
KW inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
OS Helicobacter pylori.
PN WO9737044-A1.
PD 09-OCT-1997.
PF 27-MAR-1997; U05223.
PR 06-DEC-1996; US-761318.
PR 29-MAR-1996; US-625811.
PR 02-APR-1996; US-758731.
PR 25-OCT-1996; US-736905.
PR 28-OCT-1996; US-738859.
PA (ASPR) ASPRA AB.
PI Alm RA, Smith D;
DR WPI: 97-503122/46.
DR N-PSDB: V24810.
PT Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection
PS Claim 14; Page 615; 1145pp; English.
CC This sequence is a H. pylori protein of unspecified function.
CC The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds.
CC useful as potential H. pylori life cycle activators or inhibitors. The
CC DNA and probes derived from it may be used for the identification of
CC H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
SQ Sequence 68 AA:

Query Match 4.88%; Score 6; DB 29; Length 68;
Best Local Similarity 100.0%; Pred. No. 7.37e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 32 yvlkmy 37
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OY 99 QVLKMY 104

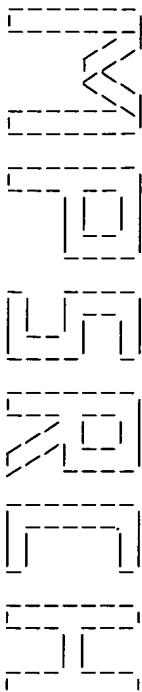
RESULT 15
ID W20697 standard; Protein: 131 AA.

AC W20697; (first entry)
DT 15-JUL-1997
DE H. pylori putative transmembrane protein 05ae20220orf51.
KW Vaccine; prevention; treatment; infection; identification;
KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope;
KW transmembrane; membrane spanning region.
OS Helicobacter pylori.
PN WO9640893-A1.
PD 19-DEC-1996.
PE 06-JUN-1996; U09122.
PR 07-JUN-1995; US-487032.
PR 01-APR-1996; US-630405.
PA (ASTR) ASTRA AB.
PI Berglinch OT, Smith D, Mellgaard BL;
DR MPI; 97-052306/05.
DR N-PSDB; T67950.
PT Helicobacter pylori nucleic acid sequences and related
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
PT infection, and to detect Helicobacter
PS Claim 73; Page 1116; 1481pp; English.
CC The present sequence represents a Helicobacter pylori protein likely
CC to contain a single membrane spanning region.
CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors.
CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping contigs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
CC production, e.g. in E. coli hosts.
SQ Sequence 131 AA;

Query Match 4.88; Score 6; DB 22; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.37e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 seqs 55
| | | | |
QY 62 SSDLFS 67

Search completed: Sat Aug 21 12:50:44 1999
Job time : 80 secs.



(TM)

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MPerch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Sat Aug 21 12:53:14 1999; MasPar time 2.46 Seconds
Tabular output not generated. 518.993 Million cell updates/sec

Title: >US-09-219-935-15
Description: (1-126) from US09219935.pep
Sequence: 1 HHQNHGHIHDESMHPIERK.....FLVFMVMDLVTLHHGH 126

Scoring table: TABLE uniprottable
Gap 60

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCR9_COMB 4:backfiles1

Statistics: Mean 2.379; Variance 0.615; scale 3.866

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	126	100.0	126	3	PCT-US92-1 Sequence 15, Applicati	5.11e-190
2	15	12.7	453	3	PCT-US92-1 Sequence 13, Applicati	1.31e-12
3	9	7.1	378	3	PCT-US92-1 Sequence 7, Applicati	7.47e-03
4	9	7.1	380	3	PCT-US92-1 Sequence 11, Applicati	7.47e-03
5	9	7.1	383	3	PCT-US94-0 Sequence 2, Applicati	7.47e-03
6	9	7.1	386	3	PCT-US92-1 Sequence 2, Applicati	7.47e-03
7	9	7.1	404	3	PCT-US92-1 Sequence 9, Applicati	7.47e-03
8	9	7.1	435	3	PCT-US94-0 Sequence 12, Applicati	7.47e-03
9	9	7.1	446	3	PCT-US92-1 Sequence 5, Applicati	7.47e-03
10	9	7.1	446	3	PCT-US94-0 Sequence 10, Applicati	7.47e-03
11	9	5.6	156	3	PCT-US92-1 Sequence 17, Applicati	2.36e+00
12	6	4.8	24	2	US-08-320- Sequence 20, Applicati	3.40e+01
13	6	4.8	24	2	US-08-320- Sequence 14, Applicati	3.40e+01
14	6	4.8	24	1	US-08-314- Sequence 20, Applicati	3.40e+01
15	6	4.8	37	2	US-08-320- Sequence 8, Applicati	3.40e+01
16	6	4.8	37	2	US-08-320- Sequence 26, Applicati	3.40e+01
17	6	4.8	40	3	PCT-US95-1 Sequence 40, Applicati	3.40e+01
18	6	4.8	101	2	US-08-190- Sequence 2, Applicati	3.40e+01
19	6	4.8	101	2	US-08-468- Sequence 2, Applicati	3.40e+01
20	6	4.8	258	3	PCT-US94-1 Sequence 1, Applicati	3.40e+01
21	6	4.8	295	3	PCT-US94-1 Sequence 6, Applicati	3.40e+01
22	6	4.8	298	3	PCT-US94-1 Sequence 2, Applicati	3.40e+01
23	6	4.8	318	1	US-08-547- Sequence 2, Applicati	3.40e+01

ALIGNMENTS

RESULT ID	1	STANDARD;	PRT;	126 AA.
XX	PCT-US92-10284-15			
XX	xxxxxx			
DE	Sequence 15, Application PC/TUS9210284			
CC	Sequence 15, Application PC/TUS9210284			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Browne, John, Kinney, Anthony J.,			
CC	APPLICANT: Pierce, John, Wierzbicki, Anna M.,			
CC	APPLICANT: Yadav, Narendra S., Perez-Grau, Luis			
CC	TITLE OF INVENTION: Fatty Acid Desaturase Genes			
CC	NUMBER OF SEQUENCES: 32			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: E. I. du Pont de Nemours and Company			
CC	STREET: 1007 Market Street			
CC	CITY: Wilmington			
CC	STATE: Delaware			
CC	COUNTRY: U.S.A.			
CC	ZIP: 19898			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: Macintosh			
CC	OPERATING SYSTEM: Macintosh System, 6.0			
CC	SOFTWARE: Microsoft Word, 4.0			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: PCT/US92/10284			
CC	FILING DATE: 19921203			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: 07/804,259			
CC	FILING DATE: 4 DECEMBER 1991			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Floyd, Linda A.			
CC	REGISTRATION NUMBER: 33,692			
CC	REFERENCE/DOCKET NUMBER: BB-1036-A			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (302) 992-4929			
CC	TELEFAX: (302) 892-7949			
CC	TELEX: 833420			
CC	INFORMATION FOR SEQ ID NO: 15:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 126 amino acids			

CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHEICAL: YES
CC FRAGMENT TYPE: internal
CC ORIGINAL SOURCE: Internal
CC ORGANISM: Zea mays
CC IMMEDIATE SOURCE:
CC CLONE: pPCR20
SQ SEQUENCE 126 AA; 14668 MW; 96232 CN;

Query Match 100.0%; Score 126; DB 3; Length 126;
Best Local Similarity 100.0%; Pred. No. 5,11e-190;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHNHGHIHRESWHPITEKLYROLEPRTKLRFTVPPPLAFVYLLYRSFGKLSHFL 60
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QY 1 HHNHGHIHRESWHPITEKLYROLEPRTKLRFTVPPPLAFVYLLYRSFGKLSHFL 60
|||
Db 61 PSSDLFSPKESDVWSTTCIMLASILAMACAFGPIQLVKMGIPLYFVMMLDVTV 120
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QY 61 PSSDLFSPKESDVWSTTCIMLASILAMACAFGPIQLVKMGIPLYFVMMLDVTV 120
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Db 121 LHHGH 126
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QY 121 LHHGH 126
|||

RESULT 2
ID PCT-US92-10284-13 STANDARD: PRT: 453 AA.
XX
AC xxxxxx
DT
DE Sequence 13, Application PC/TUS9210284
XX
CC Sequence 13, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadau, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420

CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 453 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 453 AA; 51362 MW; 1146882 CN;

Query Match 12.7%; Score 16; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 1,31e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 320 FVWMLDLYTLHHGH 335
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QY 111 FVWMLDLYTLHHGH 126
|||

RESULT 3
ID PCT-US92-10284-7 STANDARD: PRT: 378 AA.
XX
AC xxxxxx
DT
DE Sequence 7, Application PC/TUS9210284
XX
CC Sequence 7, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadau, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 378 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 378 AA; 43528 MW; 793455 CN;

Query Match 7.1%; Score 9; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 7,47e-03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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CC          GENERAL INFORMATION:
CC          APPLICANT:  Browne, John, Kinney, Anthony J.,
CC          APPLICANT:  Pierce, John, Wierzbicki, Anna M.,
CC          APPLICANT:  Yadav, Narendra S., Perez-Grau, Luis
CC          TITLE OF INVENTION:  Fatty Acid Desaturase Genes
CC          TITLE OF INVENTION:  from Plants
CC          NUMBER OF SEQUENCES:  32
CC          CORRESPONDENCE ADDRESS:
CC          ADDRESSEE:  E. I. du Pont de Nemours and Company
CC          STREET:  1007 Market Street
CC          CITY:  Wilmington
CC          STATE:  Delaware
CC          COUNTRY:  U.S.A.
CC          ZIP:  19898
CC          COMPUTER READABLE FORM:
CC          MEDIUM TYPE:  Floppy disk
CC          COMPUTER:  Macintosh
CC          OPERATING SYSTEM:  Macintosh System, 6.0
CC          SOFTWARE:  Microsoft Word, 4.0
CC          CURRENT APPLICATION DATA:
CC          APPLICATION NUMBER:  PCT/US92/10284
CC          FILING DATE:  19921203
CC          CLASSIFICATION:  435
CC          PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER:  07/804,259
CC          FILING DATE:  4 DECEMBER 1991
CC          ATTORNEY/AGENT INFORMATION:
CC          NAME:  Floyd, Linda A.
CC          REGISTRATION NUMBER:  33,692
CC          REFERENCE/DOCKET NUMBER:  BB-1036-A
CC          TELECOMMUNICATION INFORMATION:
CC          TELEPHONE:  (302) 992-4929
CC          TELEFAX:  (302) 892-7949
CC          TELEX:  835420
CC          INFORMATION FOR SEQ ID NO:  5:
CC          SEQUENCE CHARACTERISTICS:
CC          LENGTH:  446 amino acids
CC          TYPE:  AMINO ACID
CC          TOPOLOGY:  linear
CC          MOLECULE TYPE:  protein
CC          SEQ ID:  5
CC          SEQUENCE  446 AA; 51174 MW; 1094717 CN;
CC
CC          Query Match      7.1%; Score 9; DB 3; Length 446;
CC          Best Local Similarity 100.0%; Pred. No. 7.47e-03;
CC          Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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CC          Db      319 VTYLHHGH 327
CC          Oy      118 VTYLHHGH 126
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CC          RESULT      10
CC          ID      PCT-US94-01321-10      STANDARD;      PRT:      446 AA.
CC          AC      xxxxxx
CC          DT
CC          XX
CC          DE      Sequence 10, Application PC/TUS9401321
CC          XX
CC          Sequence 10, Application PC/TUS9401321
CC          CC          GENERAL INFORMATION:
CC          CC          APPLICANT:
CC          CC          TITLE OF INVENTION:  Altered Linolenic and Linoleic Acid Content
CC          CC          TITLE OF INVENTION:  in Plants
CC          CC          NUMBER OF SEQUENCES:  72
CC          CC          COMPUTER READABLE FORM:
CC          CC          MEDIUM TYPE:  Floppy disk
CC          CC          COMPUTER:  IBM PC compatible
CC          CC          OPERATING SYSTEM:  PC-DOS/MS-DOS
CC          CC          SOFTWARE:  Patentin Release #1.0, Version #1.25 (EPO)
CC          CC          CURRENT APPLICATION DATA:
CC          CC          APPLICATION NUMBER:  PCT/US94/01321

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CC      FILING DATE: 04-FEB-1994
CC      CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/156551
CC      FILING DATE: 22-NOV-1993
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/014431
CC      FILING DATE: 05-FEB-1993
CC      INFORMATION FOR SEQ ID NO: 10:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 446 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 446 AA; 51174 MW; 10947717 CN;
SQ
DB      319 VTYLHHGH 327
      |||||||
QY      118 VTYLHHGH 126

RESULT 11
ID      PCT-US92-10284-17      STANDARD;      PRT;      156 AA.
XX      xxxxxx
XX
XX
XX
XX
XX
DE      Sequence 17, Application PC/TUS9210284
XX
XX
CC      Sequence 17, Application PC/TUS9210284
CC      GENERAL INFORMATION:
CC      APPLICANT: Browse, John, Kinney, Anthony J.,
CC      APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC      APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC      TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC      TITLE OF INVENTION: from Plants
CC      NUMBER OF SEQUENCES: 32
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: E. I. du Pont de Nemours and Company
CC      STREET: 1007 Market Street
CC      CITY: Wilmington
CC      STATE: Delaware
CC      COUNTRY: U.S.A.
CC      ZIP: 19898
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: Macintosh
CC      OPERATING SYSTEM: Macintosh System, 6.0
CC      SOFTWARE: Microsoft Word, 4.0
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US92/10284
CC      FILING DATE: 19921203
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/804,259
CC      FILING DATE: 4 DECEMBER 1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Floyd, Linda A.
CC      REGISTRATION NUMBER: 33,692
CC      REFERENCE/DOCKET NUMBER: BB-1036-A
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (302) 992-4929
CC      TELEFAX: (302) 892-7949
CC      TELEX: 835420
CC      INFORMATION FOR SEQ ID NO: 17:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 156 amino acids
CC      TYPE: AMINO ACID

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CC STRANDEDNESS: unknown
 CC TOPOLOGY: unknown
 CC MOLECULE TYPE: protein
 CC HYPOTHETICAL: YES
 CC FRAGMENT TYPE: N-terminal
 CC ORIGINAL SOURCE:
 CC ORGANISM: Arabidopsis thaliana
 CC IMMEDIATE SOURCE:
 CC CLONE: pFdx-2 and pYacp7
 CC SEQUENCE 156 AA; 17771 MW; 128823 CN;
 SQ
 Query Match 5.6%; Score 7; DB 3; Length 156;
 Best Local Similarity 100.0%; Pred. No. 2.36e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 147 HHQNHGH 153
 1111111
 QY 1 HHQNHGH 7
 RESULT 12
 ID US-08-320-982-20 STANDARD; PRT; 24 AA.
 AC xxxxxx
 XX
 DT
 DE
 XX Sequence 20, Application US/08320982
 CC Sequence 20, Application US/08320982
 CC Patent No. 5801026
 CC GENERAL INFORMATION:
 CC APPLICANT: SOMERVILLE, CHRIS
 CC APPLICANT: VAN DE LOO, FRANK
 CC TITLE OF INVENTION: USE OF PLANT FATY ACYL HYDROXYLASES TO
 CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATY ACIDS AND DERIVATIVES IN PLANTS
 CC NUMBER OF SEQUENCES: 48
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
 CC STREET: 1100 NEW YORK AVENUE, N.W.
 CC CITY: WASHINGTON
 CC STATE: D.C.
 CC COUNTRY: U.S.A.
 CC ZIP: 20005
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/320,982
 CC FILING DATE: 11-OCT-1994
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/314,596
 CC FILING DATE: 26-SEP-1994
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: KOKULIS, PAUL N.
 CC REGISTRATION NUMBER: 16,773
 CC REFERENCE/DOCKET NUMBER: 206905/1220
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 202-861-3000
 CC TELEFAX: 202-822-0944
 CC INFORMATION FOR SEQ ID NO: 20:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 24 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 24 AA; 2877 MW; 3868 CN;
 SQ
 Query Match 4.8%; Score 6; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.40e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 12 FVWMD 17
 1111111
 QY 111 FVWMD 116
 RESULT 13
 ID US-08-320-982-14 STANDARD; PRT; 24 AA.
 AC xxxxxx
 XX
 DT
 DE
 XX Sequence 14, Application US/08320982
 CC Sequence 14, Application US/08320982
 CC Patent No. 5801026
 CC GENERAL INFORMATION:
 CC APPLICANT: SOMERVILLE, CHRIS
 CC APPLICANT: VAN DE LOO, FRANK
 CC TITLE OF INVENTION: USE OF PLANT FATY ACYL HYDROXYLASES TO
 CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATY ACIDS AND DERIVATIVES IN PLA
 CC NUMBER OF SEQUENCES: 48
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
 CC STREET: 1100 NEW YORK AVENUE, N.W.
 CC CITY: WASHINGTON
 CC STATE: D.C.
 CC COUNTRY: U.S.A.
 CC ZIP: 20005
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/320,982
 CC FILING DATE: 11-OCT-1994
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/314,596
 CC FILING DATE: 26-SEP-1994
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: KOKULIS, PAUL N.
 CC REGISTRATION NUMBER: 16,773
 CC REFERENCE/DOCKET NUMBER: 206905/1220
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 202-861-3000
 CC TELEFAX: 202-822-0944
 CC INFORMATION FOR SEQ ID NO: 14:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 24 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 24 AA; 2877 MW; 3868 CN;
 SQ
 Query Match 4.8%; Score 6; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.40e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 12 FVWMD 17
 1111111
 QY 111 FVWMD 116
 RESULT 14
 ID US-08-314-596-20 STANDARD; PRT; 24 AA.
 AC xxxxxx

Best Local Similarity 100.0%; Pred. No. 3.40e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 12 FVWMD 17
 1111111
 QY 111 FVWMD 116
 RESULT 13
 ID US-08-320-982-14 STANDARD; PRT; 24 AA.
 AC xxxxxx
 XX
 DT
 DE
 XX Sequence 14, Application US/08320982
 CC Sequence 14, Application US/08320982
 CC Patent No. 5801026
 CC GENERAL INFORMATION:
 CC APPLICANT: SOMERVILLE, CHRIS
 CC APPLICANT: VAN DE LOO, FRANK
 CC TITLE OF INVENTION: USE OF PLANT FATY ACYL HYDROXYLASES TO
 CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATY ACIDS AND DERIVATIVES IN PLA
 CC NUMBER OF SEQUENCES: 48
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
 CC STREET: 1100 NEW YORK AVENUE, N.W.
 CC CITY: WASHINGTON
 CC STATE: D.C.
 CC COUNTRY: U.S.A.
 CC ZIP: 20005
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/320,982
 CC FILING DATE: 11-OCT-1994
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/314,596
 CC FILING DATE: 26-SEP-1994
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: KOKULIS, PAUL N.
 CC REGISTRATION NUMBER: 16,773
 CC REFERENCE/DOCKET NUMBER: 206905/1220
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 202-861-3000
 CC TELEFAX: 202-822-0944
 CC INFORMATION FOR SEQ ID NO: 14:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 24 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 24 AA; 2877 MW; 3868 CN;
 SQ
 Query Match 4.8%; Score 6; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.40e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 12 FVWMD 17
 1111111
 QY 111 FVWMD 116
 RESULT 14
 ID US-08-314-596-20 STANDARD; PRT; 24 AA.
 AC xxxxxx

XX
DT
XX
DE Sequence 20, Application US/08314596
XX
CC Sequence 20, Application US/08314596
CC Patent No. 5668282
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentln Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 24 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 24 AA; 2877 MW; 3868 CN;
SQ

Query Match 4.88; Score 6; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.40e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 FVWMLD 17
111111
QY 111 FVWMLD 116

RESULT 15
ID US-08-320-982-8 STANDARD; PRT; 37 AA.
XX
XX
AC xxxxxx
XX
XX
DE Sequence 8, Application US/08320982
CC
CC Sequence 8, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.

CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentln Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4430 MW; 9485 CN;
SQ

Query Match 4.88; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.40e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 25 FVWMLD 30
111111
QY 111 FVWMLD 116

Search completed: Sat Aug 21 12:53:23 1999
Job time : 9 secs.

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(TM)

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Msrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:15:18 1999; Maspar time 5.60 Seconds

Tabular output not generated. 808.158 Million cell updates/sec

Title: >US-09-219-935-5

Description: (1-446) from US09219935.pep

Perfect Score: 446

Sequence: 1 MANLVSECGIRPLRIYTT.....EVYVKADPNLGEVKVRAD 446

Scoring table: TABLE uniprottable

Gap 60

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: <a-issued

1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 2.796; Variance 0.701; scale 3.989

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	446	100.0	446	3	PCT-US94-0 Sequence 10, Applicati	0.00e+00
2	446	100.0	446	3	PCT-US92-1 Sequence 5, Applicati	0.00e+00
3	103	23.1	378	3	PCT-US92-1 Sequence 7, Applicati	2.72e-154
4	103	23.1	404	3	PCT-US92-1 Sequence 9, Applicati	2.72e-154
5	43	9.6	435	3	PCT-US94-0 Sequence 3, Applicati	7.58e-43
6	36	8.1	453	3	PCT-US92-1 Sequence 13, Applicati	7.58e-43
7	31	7.0	156	3	PCT-US92-1 Sequence 17, Applicati	7.71e-35
8	28	6.3	383	3	PCT-US94-0 Sequence 2, Applicati	4.36e-30
9	28	6.3	386	3	PCT-US92-1 Sequence 2, Applicati	4.36e-30
10	27	6.1	380	3	PCT-US92-1 Sequence 11, Applicati	1.63e-28
11	25	5.6	37	2	US-08-320- Sequence 6, Applicati	2.19e-25
12	25	5.6	37	2	US-08-320- Sequence 22, Applicati	2.19e-25
13	25	5.6	37	1	US-08-314- Sequence 6, Applicati	2.19e-25
14	25	5.6	37	1	US-08-314- Sequence 22, Applicati	2.19e-25
15	22	4.9	37	1	US-08-314- Sequence 2, Applicati	2.19e-25
16	22	4.9	37	1	US-08-314- Sequence 16, Applicati	9.57e-21
17	22	4.9	37	2	US-08-320- Sequence 12, Applicati	9.57e-21
18	22	4.9	37	2	US-08-320- Sequence 16, Applicati	9.57e-21
19	18	4.0	40	2	US-08-320- Sequence 10, Applicati	1.09e-14
20	18	4.0	40	2	US-08-320- Sequence 18, Applicati	1.09e-14
21	18	4.0	40	1	US-08-314- Sequence 10, Applicati	1.09e-14
22	18	4.0	40	1	US-08-314- Sequence 18, Applicati	1.09e-14
23	12	2.7	37	1	US-08-314- Sequence 26, Applicati	4.77e-06

24	12	2.7	37	1	US-08-314- Sequence 8, Applicatio	4.77e-06
25	12	2.7	37	2	US-08-320- Sequence 8, Applicati	4.77e-06
26	12	2.7	37	2	US-08-320- Sequence 26, Applicati	4.77e-06
27	11	2.5	40	2	US-08-320- Sequence 24, Applicati	1.09e-04
28	11	2.5	40	2	US-08-320- Sequence 4, Applicati	1.09e-04
29	11	2.5	40	1	US-08-314- Sequence 4, Applicati	1.09e-04
30	11	2.5	40	1	US-08-314- Sequence 24, Applicati	1.09e-04
31	9	2.0	9	3	PCT-US94-0 Sequence 56, Applicati	4.42e-02
32	9	2.0	126	3	PCT-US92-1 Sequence 15, Applicati	4.42e-02
33	8	1.8	8	2	US-08-789- Sequence 8, Applicati	7.55e-01
34	8	1.8	8	3	PCT-US94-0 Sequence 70, Applicati	7.55e-01
35	8	1.8	8	3	PCT-US94-0 Sequence 63, Applicati	7.55e-01
36	8	1.8	20	1	US-08-607- Sequence 6, Applicati	7.55e-01
37	8	1.8	20	2	US-08-399- Sequence 6, Applicati	7.55e-01
38	8	1.8	20	1	US-08-605- Sequence 6, Applicati	7.55e-01
39	8	1.8	597	1	US-08-607- Sequence 4, Applicati	7.55e-01
40	8	1.8	597	2	US-08-961- Sequence 4, Applicati	7.55e-01
41	8	1.8	597	2	US-08-605- Sequence 4, Applicati	7.55e-01
42	8	1.8	598	1	US-08-607- Sequence 14, Applicati	7.55e-01
43	8	1.8	598	2	US-08-399- Sequence 14, Applicati	7.55e-01
44	8	1.8	598	2	US-08-605- Sequence 14, Applicati	7.55e-01
45	8	1.8	598	2	US-08-961- Sequence 14, Applicati	7.55e-01

ALIGNMENTS

RESULT	ID	Sequence	Standard	PRT	AA
1	PCT-US94-01321-10	Sequence 10, Application PC/TUS9401321			
XX	xxxxxx	GENERAL INFORMATION:			
XX		APPLICANT:			
XX		TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content			
XX		MEDIUM TYPE: In Plants			
XX		NUMBER OF SEQUENCES: 72			
XX		COMPUTER READABLE FORM:			
XX		COMPUTER: IBM PC compatible			
XX		OPERATING SYSTEM: PC-DOS/MS-DOS			
XX		SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)			
XX		CURRENT APPLICATION DATA:			
XX		APPLICATION NUMBER: PCT/US94/01321			
XX		FILING DATE: 04-FEB-1994			
XX		CLASSIFICATION:			
XX		PRIOR APPLICATION DATA:			
XX		APPLICATION NUMBER: US 08/156551			
XX		FILING DATE: 22-NOV-1993			
XX		PRIOR APPLICATION DATA:			
XX		APPLICATION NUMBER: US 08/014431			
XX		FILING DATE: 05-FEB-1993			
XX		INFORMATION FOR SEQ ID NO: 10:			
XX		SEQUENCE CHARACTERISTICS:			
XX		LENGTH: 446 amino acids			
XX		TYPE: amino acid			
XX		TOPOLOGY: linear			
XX		MOLECULE TYPE: protein			
XX		SEQUENCE 446 AA: 51174 MW; 1094717 CN;			
XX		Query Match 100.0%; Score 446; DB 3; Length 446;			
XX		Best Local Similarity 100.0%; Pred. No. 0.00e+00;			
XX		Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	1	MANLVSECGIRPLRIYTTTPRSNFTLSNNKFRPSLSSTSSSTSSPLSGFLNSRDGFTF 60			
Qy	1	MANLVSECGIRPLRIYTTTPRSNFTLSNNKFRPSLSSTSSSTSSPLSGFLNSRDGFTF 60			
Db	61	MANLVSTPLTTFEESPLEEDNKKRFDGAPPPFNLDIRAIRAHCHVKNWKSLSY 120			

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QY 61 NMAVNSPILPTTFEESPLEEDNORFDPGAPPPFNADIRAAIPKHCWKNPKSLSY 120
Db 121 VVRDVAIVFALAGAAYLNNMIWPLYLWLAOGTFMFLFVLGHDCGHSFSDPKLNSV 180
QY 121 VVRDVAIVFALAGAAYLNNMIWPLYLWLAOGTFMFLFVLGHDCGHSFSDPKLNSV 180
Db 181 GHLHSSILVYHGWIRISHRTHQNHGHNDESWHPMSEKIYNTLDKPTREFFTPLV 240
QY 181 GHLHSSILVYHGWIRISHRTHQNHGHNDESWHPMSEKIYNTLDKPTREFFTPLV 240
Db 241 MAAVFFYLMAARPGKSGSHYHPDSDLFLPKERKDVLTSTACTMAAALLVCLNFTIGIQ 300
QY 241 MAAVFFYLMAARPGKSGSHYHPDSDLFLPKERKDVLTSTACTMAAALLVCLNFTIGIQ 300
Db 301 MLKLGIPYWINVMWLDVFTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIH 360
QY 301 MLKLGIPYWINVMWLDVFTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIH 360
Db 361 HDIGTHVHNHLEFPOIPHYHLVEATEAAKPVLGKYYREBDKSGPLHLLETLAKSIKEDH 420
QY 361 HDIGTHVHNHLEFPOIPHYHLVEATEAAKPVLGKYYREBDKSGPLHLLETLAKSIKEDH 420
Db 421 YVSDGEVYVYKADPNLYGEVYKVRAD 446
QY 421 YVSDGEVYVYKADPNLYGEVYKVRAD 446
RESULT 2
ID PCT-US92-10284-5 STANDARD: PRT: 446 AA.
AC xxxxxx
XX
XX
DE Sequence 5, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: Macintosh
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A. 33,692
CC REGISTRATION NUMBER:
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC FAX: 835420
CC INFORMATION FOR SEQ ID NO: 5:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 446 AA: 51174 MW: 1094717 CN:
Query Match 100.0%; Score 446; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MANVLSGCGIRPLPRITTPRSMFLSNKKFRSLSSSTKITSSPLSFLNSRDGFT 60
QY 1 MANVLSGCGIRPLPRITTPRSMFLSNKKFRSLSSSTKITSSPLSFLNSRDGFT 60
Db 61 NMAVNSPILPTTFEESPLEEDNORFDPGAPPPFNADIRAAIPKHCWKNPKSLSY 120
QY 61 NMAVNSPILPTTFEESPLEEDNORFDPGAPPPFNADIRAAIPKHCWKNPKSLSY 120
Db 121 VVRDVAIVFALAGAAYLNNMIWPLYLWLAOGTFMFLFVLGHDCGHSFSDPKLNSV 180
QY 121 VVRDVAIVFALAGAAYLNNMIWPLYLWLAOGTFMFLFVLGHDCGHSFSDPKLNSV 180
Db 181 GHLHSSILVYHGWIRISHRTHQNHGHNDESWHPMSEKIYNTLDKPTREFFTPLV 240
QY 181 GHLHSSILVYHGWIRISHRTHQNHGHNDESWHPMSEKIYNTLDKPTREFFTPLV 240
Db 241 MAAVFFYLMAARPGKSGSHYHPDSDLFLPKERKDVLTSTACTMAAALLVCLNFTIGIQ 300
QY 241 MAAVFFYLMAARPGKSGSHYHPDSDLFLPKERKDVLTSTACTMAAALLVCLNFTIGIQ 300
Db 301 MLKLGIPYWINVMWLDVFTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIH 360
QY 301 MLKLGIPYWINVMWLDVFTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIH 360
Db 361 HDIGTHVHNHLEFPOIPHYHLVEATEAAKPVLGKYYREBDKSGPLHLLETLAKSIKEDH 420
QY 361 HDIGTHVHNHLEFPOIPHYHLVEATEAAKPVLGKYYREBDKSGPLHLLETLAKSIKEDH 420
Db 421 YVSDGEVYVYKADPNLYGEVYKVRAD 446
QY 421 YVSDGEVYVYKADPNLYGEVYKVRAD 446
RESULT 3
ID PCT-US92-10284-7 STANDARD: PRT: 378 AA.
AC xxxxxx
XX
XX
XX
DE Sequence 7, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: Macintosh
CC SOFTWARE: Microsoft Word, 4.0

RESULT 6
ID PCT-US92-10284-13 STANDARD; PRT: 453 AA.
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AC xxxxxx
XX
DT
XX
DE Sequence 13, Application PC/TUS9210284
XX
CC Sequence 13, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC City: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 453 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC QUERY MATCH 8.1%; Score 36; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 7.58e-43;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 327 VTYLHHGHEKLPYRGKESYLRGLTTLDRDYG 362
QY 319 VTYLHHGHEKLPYRGKESYLRGLTTLDRDYG 354
RESULT 7
ID PCT-US92-10284-17 STANDARD; PRT: 156 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 17, Application PC/TUS9210284
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CC Sequence 17, Application PC/TUS9210284

CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC City: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: YES
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Arabidopsis thaliana
CC IMMEDIATE SOURCE:
CC CLONE: pFad2-2 and pYacp7
SQ SEQUENCE 156 AA; 17771 MW; 128823 CN;
Query Match 7.0%; Score 31; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 7.71e-35;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 126 GHLHSSILVYHGWRISRTTHQNHGVEN 156
QY 181 GHLHSSILVYHGWRISRTTHQNHGVEN 211
RESULT 8
ID PCT-US94-01321-2 STANDARD; PRT: 383 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 2, Application PC/TUS9401321
XX
CC Sequence 2, Application PC/TUS9401321
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Lipoic and Lipoic Acid Content
CC TITLE OF INVENTION: in Plants
CC NUMBER OF SEQUENCES: 72

CC MOLECULE TYPE: peptide
SQ SEQUENCE 37 AA; 4407 MM; 7119 CN;

Query Match 4.9%; Score 22; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 9.57e-21;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIGTVIHHLFPOIPIHYHLV 22
|||
QY 360 HHDIGTVIHHLFPOIPIHYHLV 381

Search completed: Sat Aug 21 12:15:30 1999
Job time : 12 secs.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 22, 1999, 05:27:58 ; Search time 82.1 seconds
(without alignments)
284.744 Million cell updates/sec

Title: US-09-219-935-3

Perfect score: 255
Sequence: 1 AAATTCATCAACCCCTTCT.....GCGATCTCAAGACAGCTGTG 255

Scoring table: OLIGO_NUC

Searched: 176461 seqs, 45838279 residues

Database: Issued_Patents_NA:*

- 1: /cgn1_6/ptodata/2/1na/5A.COMB.seq:*
- 2: /cgn1_6/ptodata/2/1na/5B.COMB.seq:*
- 3: /cgn1_6/ptodata/2/1na/5C.COMB.seq:*
- 4: /cgn1_6/ptodata/2/1na/5D.COMB.seq:*
- 5: /cgn1_6/ptodata/2/1na/PTUS9.COMB.seq:*
- 6: /cgn1_6/ptodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	255	100.0	255	5	PCT-US92-10284-3
2	188	73.7	1350	5	PCT-US92-10284-1
3	35	13.7	1353	5	PCT-US94-01321-1
4	22	8.6	3083	1	US-07-718-575-5
5	22	8.6	3083	3	US-08-481-206-5
6	21	8.2	329	2	US-08-253-155A-73
7	19	7.5	1800	3	US-08-848-252-3
8	18	7.1	1491	2	US-08-468-853-1
9	18	7.1	3958	2	US-08-435-933-5
10	18	7.1	43	2	US-08-473-096-1
11	18	7.1	43	2	US-08-473-096-2
12	18	7.1	43	2	US-08-473-096-3
13	18	7.1	43	2	US-08-473-096-4
14	18	7.1	43	2	US-08-473-096-5
15	18	7.1	43	2	US-08-473-096-11
16	18	7.1	43	2	US-08-473-096-12
17	18	7.1	1491	3	US-08-468-855-1
18	18	7.1	1491	3	US-08-310-357-1
19	18	7.1	1491	3	US-08-468-852-1
20	18	7.1	614	4	US-08-692-787-2
21	18	7.1	3958	5	PCT-US96-06035-5
22	17	6.7	1978	1	US-07-753-520B-2
23	17	6.7	9115	1	US-07-753-520B-3
24	17	6.7	8316	1	US-07-753-520B-4
25	17	6.7	243	1	US-07-922-723A-9
26	17	6.7	243	1	US-07-799-828C-9
27	17	6.7	243	1	US-08-074-275-9
28	17	6.7	552	1	US-08-222-177A-418
29	17	6.7	2263	1	US-08-176-126B-1
30	17	6.7	893	2	US-08-276-452A-66
31	17	6.7	1157	2	US-08-215-083-1
32	17	6.7	150	2	US-08-314-596-30
33	17	6.7	104	2	US-08-314-596-31
34	17	6.7	1448	2	US-08-314-596-32
35	17	6.7	1018	2	US-08-314-596-33
36	17	6.7	243	2	US-08-480-366-9
37	17	6.7	1668	2	US-08-471-791-15

ALIGNMENTS

38	17	6.7	26700	2	US-08-472-217-1	Sequence 1, Appl
39	17	6.7	2520	3	US-08-405-254-9	Sequence 9, Appl
40	17	6.7	150	3	US-08-320-982-30	Sequence 30, Appl
41	17	6.7	104	3	US-08-320-982-31	Sequence 31, Appl
42	17	6.7	1448	3	US-08-320-982-39	Sequence 39, Appl
43	17	6.7	3402	3	US-08-480-917-1	Sequence 1, Appl
44	17	6.7	893	4	US-08-798-744-66	Sequence 66, Appl
45	17	6.7	3892	4	US-08-555-723B-3	Sequence 3, Appl

RESULT 1
PCT-US92-10284-3
Sequence 3, Application PC/TUS9210284

GENERAL INFORMATION:

APPLICANT: Browse, John, Kinney, Anthony J.,
APPLICANT: Pierce, John, Wierzbicki, Anna M.,
APPLICANT: Yadav, Narendra S., Perez-Grau, Luis

TITLE OF INVENTION: Fatty Acid Desaturase Genes

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington

STATE: Delaware

COUNTRY: U.S.A.

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: Macintosh System, 6.0

SOFTWARE: Microsoft word, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10284

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/804,259

FILING DATE: 4 DECEMBER 1991

ATTORNEY/AGENT INFORMATION:

NAME: Floyd, Linda A.

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: BB-1036-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 992-4929

TELEFAX: (302) 892-7949

TELEX: 835420

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 255 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Arabidopsis thaliana

IMMEDIATE SOURCE:

CLONE: pF1

FEATURE:

NAME/KEY: exon

LOCATION: 68..255

PCT-US92-10284-3

Query Match 100.0%; Score 255; DB 5; Length 255;

Best Local Similarity 100.0%; Pred. No. 2,4e-121;

Matches 255; Conservative 0; Mismatches 0; Gaps 0;

1 AAATTCATCAACCCCTTCTTACCAATTTTTCACGTGAGCGCATTAACATTTTGAGA 60

APPLICANT: Heltemann Ph.D., Stephen F.
APPLICANT: Boulter Ph.D., James R.
APPLICANT: Hollmann Ph.D., Michael MN
APPLICANT: Bettler Ph.D., Bernhard MN
APPLICANT: Jensen Ph.D., Jan E.
TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: United States
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/718,575
FILING DATE: 19910813
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
TELEX: 910330318
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: GLUR3
FEATURE:
NAME/KEY: CDS
LOCATION: 167..2833
US-07-718-575-5

Query Match 8.6%; Score 22; DB 1; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTCTCTC 89
DB 36 CTCCTCTCTCTCTCTCTCTC 57

RESULT 5
US-08-481-206-5
Sequence 5, Application US/08481206
Patent No. 5739291
GENERAL INFORMATION:
APPLICANT: Heltemann Ph.D., Stephen F.
APPLICANT: Boulter Ph.D., James R.
APPLICANT: Hollmann Ph.D., Michael MN
APPLICANT: Bettler Ph.D., Bernhard MN
APPLICANT: Jensen Ph.D., Jan E.
TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles

STATE: California
COUNTRY: United States
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,206
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/013,767
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
TELEX: 910330318
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: GLUR3
FEATURE:
NAME/KEY: CDS
LOCATION: 167..2833
US-08-481-206-5

Query Match 8.6%; Score 22; DB 3; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTCTCTC 89
DB 36 CTCCTCTCTCTCTCTCTCTC 57

RESULT 6
US-08-253-155A-23/C
Sequence 23, Application US/08253155A
Patent No. 5691147
GENERAL INFORMATION:
APPLICANT: Gyuris, Jenio
APPLICANT: Diasteta, Giulio
TITLE OF INVENTION: CDK4 Binding Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155A
FILING DATE: 02-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

LIBRARY: Mouse;

```

; SINGLEDNESS: 000000
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

```

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      CLONE: M/69-J1ld Heat-Stable Antigen
      FEATURE:
      NAME/KEY: sig_peptide
      LOCATION: 73..150
      FEATURE:
      NAME/KEY: mat_peptide
      LOCATION: 151..300
      FEATURE:
      NAME/KEY: CDS
      LOCATION: 73..303
      US-08-848-252-3

Query Match      7.5%; Score 19; DB 3; Length 1800;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      68 CTCCTCTCTCTCTCTCTCT 86
          |||
Db      269 CTCCTCTCTCTCTCTCTCT 287

RESULT      8
US-08-468-853-1
; Sequence 1, Application US/08468853
; Patent No. 5670362
; GENERAL INFORMATION:
; APPLICANT: van den BOOGAART, Paul
; APPLICANT: KOK, Jacobus Johannes
; APPLICANT: VERMEULEN, Arnoldus Nicolaas
; TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5670362el Patent Department
; STREET: 1300 Piccard Drive
; City: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,853
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,357
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,865
; FILING DATE: 06-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/604,075
; FILING DATE: 18-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91.201.523.7
; FILING DATE: 18-Jun-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary E. Gornley
; REGISTRATION NUMBER: 34,409
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1491 base pairs
; type: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

```

FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Elmeria acerulina
INDIVIDUAL ISOLATE: Merozoites
IMMEDIATE SOURCE:
LIBRARY: Merozoites cdna lambda gt11
CLONE: Bam200
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1344
US-08-468-853-1

Query Match 7.1%; Score 18; DB 2; Length 1491;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 CTCCTCCGCGATGCTGT 120
|||||
DB 346 CTCCTCCGCGATGCTGT 363

RESULT 9
US-08-435-933-5
Sequence 5, Application US/08435933
Patent No. 5693492
GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
APPLICANT: Pares, Philip S.
APPLICANT: Liu, Ken K.
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,933
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, III John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-435-933-5

Query Match 7.1%; Score 18; DB 2; Length 3958;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 68 CTCCTCTCTCTCTCTTC 85
|||||

DB 3307 CTCCTCTCTCTCTCTTC 3324

RESULT 10
US-08-473-096-1
Sequence 1, Application US/08473096
Patent No. 5693773
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Triplex-Forming Antisense
TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting
TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
TITLE OF INVENTION: and Pyrimidines
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect for Windows 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,096
FILING DATE: June 7, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 95,606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 monomers
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOETHERICAL: NO
ANTI-SENSE: YES
US-08-473-096-1

Query Match 7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 68 CTCCTCTCTCTCTCTTC 85
|||||
DB 16 CTCCTCTCTCTCTCTTC 33

RESULT 11
US-08-473-096-2
Sequence 2, Application US/08473096
Patent No. 5693773
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Triplex-Forming Antisense
TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting
TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
TITLE OF INVENTION: and Pyrimidines
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000

```

: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect for Windows 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/473,096
: FILING DATE: June 7, 1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Greenfield, Michael S.
: REGISTRATION NUMBER: 37,142
: REFERENCE/DOCKET NUMBER: 95,606
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)715-1000
: TELEFAX: (312)715-1234
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 43 monomers
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: HYPOTHEITICAL: NO
: ANTI-SENSE: YES
: US-08-473-096-2

Query Match      7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTTC 85
DB 16 CTCCTCTCTCTCTCTTC 33

RESULT 12
US-08-473-096-3
: Sequence 3, Application US/08473096
: Patent No. 5693773
: GENERAL INFORMATION:
: APPLICANT: Kandimala, Ekambar R.
: TITLE OF INVENTION: Triplex-Forming Antisense
: TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting
: TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner & Allegretti, Ltd.
: STREET: 10 S. Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect for Windows 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/473,096
: FILING DATE: June 7, 1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Greenfield, Michael S.
: REGISTRATION NUMBER: 37,142
: REFERENCE/DOCKET NUMBER: 95,606
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)715-1000
: TELEFAX: (312)715-1234
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 43 monomers
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: HYPOTHEITICAL: NO
: ANTI-SENSE: YES
: US-08-473-096-4
```

```

: TELEPHONE: (312)715-1000
: TELEFAX: (312)715-1234
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 43 monomers
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: HYPOTHEITICAL: NO
: ANTI-SENSE: YES
: US-08-473-096-3

Query Match      7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTTC 85
DB 16 CTCCTCTCTCTCTCTTC 33

RESULT 13
US-08-473-096-4
: Sequence 4, Application US/08473096
: Patent No. 5693773
: GENERAL INFORMATION:
: APPLICANT: Kandimala, Ekambar R.
: TITLE OF INVENTION: Triplex-Forming Antisense
: TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting
: TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner & Allegretti, Ltd.
: STREET: 10 S. Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect for Windows 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/473,096
: FILING DATE: June 7, 1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Greenfield, Michael S.
: REGISTRATION NUMBER: 37,142
: REFERENCE/DOCKET NUMBER: 95,606
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)715-1000
: TELEFAX: (312)715-1234
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 43 monomers
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: HYPOTHEITICAL: NO
: ANTI-SENSE: YES
: US-08-473-096-4

Query Match      7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTTC 85
```

Db 16 CTCCTCTCTCTCTCTC 33

RESULT 14

US-08-473-096-5
Sequence 5, Application US/08473096
Patent No. 5693773

GENERAL INFORMATION:

APPLICANT: Kandimala, Ekambar R.

TITLE OF INVENTION: Triplex-Forming Antisense

TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting

TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd

STREET: 10 S. Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect for Windows 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,096

FILING DATE: June 7, 1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Greenfield, Michael S.

REGISTRATION NUMBER: 37,142

REFERENCE/DOCKET NUMBER: 95,606

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)715-1000

TELEFAX: (312)715-1234

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 monomers

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

HYPOTHEICAL: NO

ANTI-SENSE: YES

US-08-473-096-5

Query Match 7.1%; Score 18; DB 2; Length 43;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTC 85

Db 16 CTCCTCTCTCTCTCTC 33

RESULT 15

US-08-473-096-11

Sequence 11, Application US/08473096

Patent No. 5693773

GENERAL INFORMATION:

APPLICANT: Kandimala, Ekambar R.

TITLE OF INVENTION: Triplex-Forming Antisense

TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting

TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 S. Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect for Windows 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,096

FILING DATE: June 7, 1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Greenfield, Michael S.

REGISTRATION NUMBER: 37,142

REFERENCE/DOCKET NUMBER: 95,606

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)715-1000

TELEFAX: (312)715-1234

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 monomers

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

HYPOTHEICAL: NO

ANTI-SENSE: YES

US-08-473-096-11

Query Match 7.1%; Score 18; DB 2; Length 43;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTC 85

Db 16 CTCCTCTCTCTCTCTC 33

Search completed: August 22, 1999, 05:28:01

Job time: 3639 sec

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APPLICANT: Simard, Jacques
 APPLICANT: Emi, Mitsuru
 APPLICANT: Nakamura, Yusuke
 APPLICANT: Durocher, Francine
 TITLE OF INVENTION: 17q-linked Breast and Ovarian Cancer
 TITLE OF INVENTION: Susceptibility Gene
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 STREET: 1201 New York Avenue, N.W., Suite 1000
 City: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,002
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/409,305
 FILING DATE: 24-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/348,824
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/308,104
 FILING DATE: 16-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/300,266
 FILING DATE: 02-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/289,221
 FILING DATE: 12-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24884-109347
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 513 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-487-002-19

Query Match 1.6%; Score 22; DB 2; Length 513;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1300 TCTTTTCTTTCTTTCTTTT 1321
 DB 316 TCTTTTCTTTCTTTCTTTT 337
 RESULT 8
 US-08-481-206-5
 Sequence 5, Application US/08481206
 Patent No. 5739291
 GENERAL INFORMATION:

APPLICANT: Heinemann Ph.D., Stephen F.
 APPLICANT: Boulter Ph.D., James R.
 APPLICANT: Hollmann Ph.D., Michael NMN
 APPLICANT: Bettler Ph.D., Bernhard NMN
 TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND
 TITLE OF INVENTION: METHODS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 STREET: 444 So. Flower St., Suite 2000
 City: Los Angeles
 STATE: California
 COUNTRY: United States
 ZIP: 90071-2921
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/481,206
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/013,767
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Reiter Ph.D., Stephen E.
 REGISTRATION NUMBER: 31192
 REFERENCE/DOCKET NUMBER: P31 8962
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 TELEX: 910330318
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3083 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 CLONE: Glur3
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 167..2833
 US-08-481-206-5

Query Match 1.6%; Score 22; DB 3; Length 3083;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCCTCTCTCTCTCTCTCTC 22
 DB 36 CTCCTCTCTCTCTCTCTCTC 57
 RESULT 9
 US-08-483-554B-19
 Sequence 19, Application US/08483554B
 Patent No. 5747282
 GENERAL INFORMATION:
 APPLICANT: Skolnick, Mark H.
 APPLICANT: Goldgar, David E.
 APPLICANT: Mikl, Yoshio
 APPLICANT: Swenson, Jeff
 APPLICANT: Kamb, Alexander
 APPLICANT: Harsman, Keith D.
 APPLICANT: Shattuck-Eidens, Donna M.
 APPLICANT: Tavligian, Sean V.
 APPLICANT: Wiseman, Roger W.

```

1  APPLICANT: Futreal, P. Andrew
2  TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
3  TITLE OF INVENTION: Susceptibility Gene
4  NUMBER OF SEQUENCES: 85
5  CORRESPONDENCE ADDRESSES:
6  ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
7  STREET: 1201 New York Avenue, N.W., Suite 1000
8  CITY: Washington
9  STATE: DC
10 COUNTRY: USA
11 ZIP: 20005
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/483,554B
19 FILING DATE: 07-JUN-1995
20 CLASSIFICATION: 514
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 08/409,305
23 FILING DATE: 24-MAR-1995
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/348,824
26 FILING DATE: 29-NOV-1994
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 08/308,104
29 FILING DATE: 16-SEP-1994
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 08/300,266
32 FILING DATE: 02-SEP-1994
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: US 08/289,221
35 FILING DATE: 12-AUG-1994
36 ATTORNEY/AGENT INFORMATION:
37 NAME: Ihnen, Jeffrey L.
38 REGISTRATION NUMBER: 28,957
39 REFERENCE/DOCKET NUMBER: 24884-109347
40 TELECOMMUNICATION INFORMATION:
41 TELEPHONE: 202-962-4810
42 TELEFAX: 202-962-8300
43 INFORMATION FOR SEQ ID NO: 19:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 513 base pairs
46 TYPE: nucleic acid
47 STRANDEDNESS: double
48 TOPOLOGY: linear
49 MOLECULE TYPE: DNA (genomic)
50 HYPOTHEetical: NO
51 ANTI-SENSE: NO
52 ORIGINAL SOURCE:
53 ORGANISM: Homo sapiens
54 US-08-483-554B-19

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Query Match      1.6%; Score 22; DB 3; Length 513;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY   1300 TCTTTTTTTTCTTTTTTTTT 1321
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Db    316 TCTTTTTTTTCTTTTTTTTT 337

RESULT 10
US-08-488-011B-19
; Sequence 19, Application US/08488011B
; Patent No. 5753441
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
```

APPLICANT: Swenson, Jeff
 APPLICANT: Kamb, Alexander
 APPLICANT: Harshman, Keith D.
 APPLICANT: Shattuck-Eidens, Donna M.
 APPLICANT: Tavtiglian, Sean V.
 APPLICANT: Wiseman, Roger W.
 APPLICANT: Futreal, P. Andrew
 TITLE OF INVENTION: 17q-linked Breast and Ovarian Cancer
 TITLE OF INVENTION: Susceptibility Gene
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,011B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/409,305
 FILING DATE: 24-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/348,824
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/308,104
 FILING DATE: 16-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/300,266
 FILING DATE: 02-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/289,221
 FILING DATE: 12-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24884-109347-09
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 513 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 JS-08-488-011B-19

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Query Match      1.6%; Score 22; DB 3; Length 51;
Best Local Similarity 100.0%; Pred.No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1300 TCTTTTTCGTTTTTTT 1321
      |||
Db    316 TCATTTTTCATTTT 337

RESULT 11
OS-08-644-664B-31
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; Sequence 31, Application US/08644664B
; Patent No. 5776746
; GENERAL INFORMATION:
; APPLICANT: Denny Jr., Dan W.
; TITLE OF INVENTION: Gene Amplification Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,664B
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: GENOTOPE-00912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..186
; US-08-644-664B-31

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Query Match 1.6%; Score 22; DB 3; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1030 TTGGAGATACACAGAAC 1051
DB 54 TTGGAGATACACAGAAC 75

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RESULT 12
PCT-US95-10202-19
; Sequence 19, Application PC/TUS9510202
; GENERAL INFORMATION:
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Simard, Jacques
; APPLICANT: Emi, Mitsuru
; APPLICANT: Nakamura, Yusuke
; TITLE OF INVENTION: In Vivo Mutations and Polymorphisms
; TITLE OF INVENTION: In the 17q-Linked Breast and Ovarian Cancer
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Beetler, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08-308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PCT-US95-10202-19

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Query Match 1.6%; Score 22; DB 5; Length 513;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1300 TCTTTTCTTTCTTTT 1321
DB 316 TCTTTTCTTTCTTTT 337

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RESULT 13
PCT-US95-10203-19
; Sequence 19, Application PC/TUS9510203
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10203
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08-308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-10203-19

Query Match 1.6%; Score 22; DB 5; Length 513;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1300 TCTTTTCTTTCTTTCTTTCTTTT 1321
|||||
Db 316 TCTTTTCTTTCTTTCTTTCTTTT 337

RESULT 14
PCT-US95-10220-19
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.

APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavligian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: Method for Diagnosing a
TITLE OF INVENTION: Predisposition for Breast and Ovarian Cancer
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10220
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08-308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-10220-19

Query Match 1.6%; Score 22; DB 5; Length 513;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1300 TCTTTTCTTTCTTTCTTTCTTTT 1321
|||||
Db 316 TCTTTTCTTTCTTTCTTTCTTTT 337

RESULT 15
US-08-312-312A-1

Search completed: August 22, 1999, 05:27:58
Job time: 3636 sec

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: Sequence 1, Application US/08312312A
: Patent No. 5550024
: GENERAL INFORMATION:
: APPLICANT: Rothschild, Max F.
: APPLICANT: Tuggle, Christopher K.
: APPLICANT: Jacobson, Carol D.
: APPLICANT: Mileham, Alan J.
: APPLICANT: Plastow, Graham S.
: APPLICANT: Vaske, David A.
: TITLE OF INVENTION: Genetic Markers for Pig Litter Size
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
: STREET: 801 Grand Suite 3200
: CITY: Des Moines
: STATE: Iowa
: COUNTRY: United States
: ZIP: 50309
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/312,312A
: FILING DATE: 26-SEP-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/961,819
: FILING DATE: 19-OCT-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/687,708
: FILING DATE: 19-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Nebel, Heidi S.
: REGISTRATION NUMBER: 37,719
: REFERENCE/DOCKET NUMBER: BRDC-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 515-288-3667
: TELEFAX: 515-288-1338
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3460 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 303..304
: OTHER INFORMATION: /note- "Gap in DNA sequence of
: OTHER INFORMATION: undetermined length"
: FEATURE:
: NAME/KEY: exon
: LOCATION: 534..600
: US-08-312-312A-1

```

```

Query Match 1.6%; Score 21; DB 1; Length 3460;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1297 AACCTTTTTCCTTTT 1317
DB 3041 AACCTTTTTCCTTTT 3061

```

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